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OM protein - protein search, using sw model

Run on: July 23, 2001, 13:22:06 ; Search time 20.3 Seconds
(without alignments)
907.997 Million cell updates/sec

Title: US-09-483-831-69
Perfect score: 5019
Sequence: 1 MARRSFQSCQISLFTFAV.....RSYPILTLKTLHTVESEI 915

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5019	100.0	915	1	US-08-346-455B-69
2	5019	100.0	915	3	US-08-977-221-69
3	5019	100.0	915	5	PCT-US95-06613-69
4	4533	90.3	829	1	US-08-346-455B-34
5	4533	90.3	829	3	US-08-977-221-34
6	4533	90.3	829	5	PCT-US95-06613-34
7	4418	88.0	861	1	US-08-346-455B-67
8	4418	88.0	861	3	US-08-977-221-67
9	4418	88.0	861	5	PCT-US95-06613-67
10	4279	85.3	979	1	US-08-346-455B-38
11	4279	85.3	979	3	US-08-977-221-38
12	4279	85.3	979	5	PCT-US95-06613-38
13	3842	76.5	788	1	US-08-346-455B-36
14	3842	76.5	788	3	US-08-977-221-36
15	3842	76.5	788	5	PCT-US95-06613-36
16	1955.5	39.0	873	3	US-09-187-331-6
17	1955.5	39.0	925	2	US-08-332-946-1
18	1955.5	39.0	925	2	US-08-504-169-1
19	1955.5	39.0	925	5	PCT-US94-14893-1
20	360	7.2	438	3	US-09-187-331-2
21	357	7.1	355	2	US-09-014-969-19
22	192	3.8	39	1	US-08-346-455B-54
23	192	3.8	39	3	US-08-977-221-54
24	192	3.8	39	5	PCT-US95-06613-54
25	126.5	2.5	2471	4	US-09-112-450-4
26	123	2.5	4654	4	US-08-476-515A-84
27	123	2.5	4655	4	US-08-652-877-84

28	123	2.5	4655	4	US-08-652-877-88	Sequence 88, Appl
29	123	2.5	4655	4	US-08-652-877-90	Sequence 90, Appl
30	123	2.4	4655	4	US-08-652-877-86	Sequence 86, Appl
31	118	2.4	23	1	US-07-822-043-11	Sequence 11, Appl
32	115	2.3	1833	3	US-08-479-722B-2	Sequence 2, Appl
33	115	2.3	1833	5	PCT-US95-02251-18	Sequence 18, Appl
34	113	2.3	22	1	US-07-822-043-33	Sequence 33, Appl
35	113	2.3	22	1	US-08-346-455B-33	Sequence 33, Appl
36	113	2.3	22	3	US-08-977-221-33	Sequence 33, Appl
37	113	2.3	22	5	PCT-US95-06613-33	Sequence 33, Appl
38	112	2.2	1394	6	5177197-30	Patent No. 5177197
39	110	2.2	23	1	US-08-346-455B-11	Sequence 11, Appl
40	110	2.2	23	3	US-08-977-221-11	Sequence 11, Appl
41	110	2.2	23	5	PCT-US95-06613-11	Sequence 11, Appl
42	109.5	2.2	1810	5	PCT-US95-11684-4	Sequence 4, Appl
43	108	2.2	465	3	US-08-701-582B-13	Sequence 13, Appl
44	108	2.2	465	3	US-09-063-893A-19	Sequence 19, Appl
45	107.5	2.1	605	4	US-09-042-785A-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-346-455B-69
; Sequence 69, Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,455B
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: CDNA

; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: A2058 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; US-08-346-455B-69

Query Match 100.0%; Score 5019; DB 1; Length 915;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSFQSCQIIISLFTFAVGSICLGFTHAHRKRAEGWEEGPTVLSDSPWNTNIGSCK 60
DB 1 MARRSFQSCQIIISLFTFAVGSICLGFTHAHRKRAEGWEEGPTVLSDSPWNTNIGSCK 60

QY 61 GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKRCGEVRNEENACHC 120
DB 61 GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKRCGEVRNEENACHC 120

QY 121 SEDCLARGDCTNYQVCKGESHWDDECEIKAAECPAGFVRPPLIIFSVGDFRASVMK 180
DB 121 SEDCLARGDCTNYQVCKGESHWDDECEIKAAECPAGFVRPPLIIFSVGDFRASVMK 180

QY 181 KGSVMPNIEKLRSCGTHSPYMPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
DB 181 KGSVMPNIEKLRSCGTHSPYMPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240

QY 241 TFHLRGKFNHRWGGQPLWITATKQVAGTFWVSWIPHERRIITILRWLTLPDHER 300
DB 241 TFHLRGKFNHRWGGQPLWITATKQVAGTFWVSWIPHERRIITILRWLTLPDHER 300

QY 301 PSYATYSEQDPSGHKYGPGPESSYSGPFTPAKRPKRKVPAPKRRR 360
DB 301 PSYATYSEQDPSGHKYGPGPESSYSGPFTPAKRPKRKVPAPKRRR 360

QY 361 KIHRMDHYAAETRODKMTNPLREIDKIVGQMLDGLKQLKLRRCVNVIFVGDHGMEDVTC 420
DB 361 KIHRMDHYAAETRODKMTNPLREIDKIVGQMLDGLKQLKLRRCVNVIFVGDHGMEDVTC 420

QY 421 RTEFLSNLTNVDITLVPOTGLRIRSKFSNNAKYDPKAIITANLTCCKPDQHFPRYLKQH 480
DB 421 RTEFLSNLTNVDITLVPOTGLRIRSKFSNNAKYDPKAIITANLTCCKPDQHFPRYLKQH 480

QY 481 LPKRLHYANNRRIEDIHLVERHWHVARKPLDVYKPSGKCFQGDHGFNDKNSMQTVF 540
DB 481 LPKRLHYANNRRIEDIHLVERHWHVARKPLDVYKPSGKCFQGDHGFNDKNSMQTVF 540

QY 541 VGYGPTFKYTKYPPFFENIELYNWCDLLGLKPAPNNGTHGSLNHLRTNTFRPTMPREV 600
DB 541 VGYGPTFKYTKYPPFFENIELYNWCDLLGLKPAPNNGTHGSLNHLRTNTFRPTMPREV 600

QY 601 TRPNYPGIMYLSQSDFLGCTCDDKVEPKNLDELNKLHRTKGSTERHLLYGRPAVLYRT 660
DB 601 TRPNYPGIMYLSQSDFLGCTCDDKVEPKNLDELNKLHRTKGSTERHLLYGRPAVLYRT 660

QY 661 RYDILYHTDFESGYSEITFLLMLWTSYVSKQAEVSSVPDHLTSCVRPDVRSFQSNCL 720
DB 661 RYDILYHTDFESGYSEITFLLMLWTSYVSKQAEVSSVPDHLTSCVRPDVRSFQSNCL 720

QY 721 AYKNDKMSYGFELPPYLSSSPEAKYDAFLVTNNMVPYPAFKRVNMYFORVLVKYASER 780
DB 721 AYKNDKMSYGFELPPYLSSSPEAKYDAFLVTNNMVPYPAFKRVNMYFORVLVKYASER 780

QY 781 NGYNVISGPIFDYDGLHDTEDIKQYVEGSSIPVTHYYSITSLDFTQPADKCDGP 840
DB 781 NGYNVISGPIFDYDGLHDTEDIKQYVEGSSIPVTHYYSITSLDFTQPADKCDGP 840

QY 841 LSVSSFTLPHRPDNEESCNSDESKVWEELMKMHTARVRDIEHLTSLDFFPKTSRSTPE 900
DB 841 LSVSSFTLPHRPDNEESCNSDESKVWEELMKMHTARVRDIEHLTSLDFFPKTSRSTPE 900

QY 901 ILTLKTYLHTYESEI 915
DB 901 ILTLKTYLHTYESEI 915

RESULT 2
US-08-977-221-69
; Sequence 69, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-41490S3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-8849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: A2058 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; US-08-977-221-69

Query Match 100.0%; Score 5019; DB 3; Length 915;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSFQSCQIIISLFTFAVGSICLGFTHAHRKRAEGWEEGPTVLSDSPWNTNIGSCK 60
DB 1 MARRSFQSCQIIISLFTFAVGSICLGFTHAHRKRAEGWEEGPTVLSDSPWNTNIGSCK 60

QY 61 GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKRCGEVRNEENACHC 120

Db 61 GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKRCGEVRNEENACHC 120
QY 121 SEDCLARGDCCTNYQVCKGESHVDDCEETKAACPCAGFVRPPLIIFSVDFRASYMK 180
Db 121 SEDCLARGDCCTNYQVCKGESHVDDCEETKAACPCAGFVRPPLIIFSVDFRASYMK 180
QY 181 KGSKVPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFA 240
Db 181 KGSKVPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFA 240
QY 241 TFHLRGREKFNHRWGGQPLWITATQGVKAGTFWVSWVPIPHERRILTLRLWTLDPDHER 300
Db 241 TFHLRGREKFNHRWGGQPLWITATQGVKAGTFWVSWVPIPHERRILTLRLWTLDPDHER 300
QY 301 PSVAFYSEQPDFSGHKYGPFGPESSYSGSPPTPAKPRKRVAPKRRQRPVAPPKRRR 360
Db 301 PSVAFYSEQPDFSGHKYGPFGPESSYSGSPPTPAKPRKRVAPKRRQRPVAPPKRRR 360
QY 361 KIRMDHYAAETRODKMNPRLREIDKIVGOLMDGLKOLKLRRCVNVIFVGDHGMEDVTC 420
Db 361 KIRMDHYAAETRODKMNPRLREIDKIVGOLMDGLKOLKLRRCVNVIFVGDHGMEDVTC 420
QY 421 RTEFLSNLTNVDDITLVPGLGRIRSKFSNNAKYDPKAIANLTCKPDQHFVKYKQH 480
Db 421 RTEFLSNLTNVDDITLVPGLGRIRSKFSNNAKYDPKAIANLTCKPDQHFVKYKQH 480
QY 481 LPKRLHYANNRIEDIHLLVERRHVARKPLDYKKPSCKCFQGDHGFNDKNSMQTVF 540
Db 481 LPKRLHYANNRIEDIHLLVERRHVARKPLDYKKPSCKCFQGDHGFNDKNSMQTVF 540
QY 541 VGYGTFKYKVPFENIELYNVMDLGLKAPNNGTHGSLNHLRLTNTFRPTMPEV 600
Db 541 VGYGTFKYKVPFENIELYNVMDLGLKAPNNGTHGSLNHLRLTNTFRPTMPEV 600
QY 601 TRPNYGYIMYLQSDFDLCTCDDKVEPKNKLDELNKLHRTKSTEEHLLYGRPAVLYRT 660
Db 601 TRPNYGYIMYLQSDFDLCTCDDKVEPKNKLDELNKLHRTKSTEEHLLYGRPAVLYRT 660
QY 661 RYDILYHDFESGYSEIFLMLLWTSYVSKQAEVSPDHLTSCVRPDRVSPFSQNC 720
Db 661 RYDILYHDFESGYSEIFLMLLWTSYVSKQAEVSPDHLTSCVRPDRVSPFSQNC 720
QY 721 AYKNDKQMSYGLFPPLYLSSPEAKYDAFLVTNMPYPAFKRVNMYFORVLVKKYASER 780
Db 721 AYKNDKQMSYGLFPPLYLSSPEAKYDAFLVTNMPYPAFKRVNMYFORVLVKKYASER 780
QY 781 NGVNVISGPIFDYDGLHDEDKIKQVVEGSSIPVPTHYYSITSCLDFTOPADKCDGP 840
Db 781 NGVNVISGPIFDYDGLHDEDKIKQVVEGSSIPVPTHYYSITSCLDFTOPADKCDGP 840
QY 841 LSVSFFILPHRDNESCSSEDESKWVEELMKMTARVRDIEHLTSLDFFRKTSRYPE 900
Db 841 LSVSFFILPHRDNESCSSEDESKWVEELMKMTARVRDIEHLTSLDFFRKTSRYPE 900
QY 901 ILTKLTYLHTYESEI 915
Db 901 ILTKLTYLHTYESEI 915

RESULT 3
PCT-US95-06613-69
; Sequence 69, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRI; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 915
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: A2058 ATX protein
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PCT-US95-06613-69

Query Match 100.0%; Score 5019; DB 5; Length 915;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARRSSFQSCQIIISLFTFAVGVSICLGTAAHRIKRAEGWEEGPPTVLSDSPTWISGSK 60
Db 1 MARRSSFQSCQIIISLFTFAVGVSICLGTAAHRIKRAEGWEEGPPTVLSDSPTWISGSK 60
QY 61 GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKRCGEVRNEENACHC 120
Db 61 GRCFELQAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKRCGEVRNEENACHC 120
QY 121 SEDCLARGDCCTNYQVCKGESHVDDCEETKAACPCAGFVRPPLIIFSVDFRASYMK 180
Db 121 SEDCLARGDCCTNYQVCKGESHVDDCEETKAACPCAGFVRPPLIIFSVDFRASYMK 180
QY 181 KGSKVPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFA 240
Db 181 KGSKVPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFA 240
QY 241 TFHLRGREKFNHRWGGQPLWITATQGVKAGTFWVSWVPIPHERRILTLRLWTLDPDHER 300
Db 241 TFHLRGREKFNHRWGGQPLWITATQGVKAGTFWVSWVPIPHERRILTLRLWTLDPDHER 300
QY 301 PSVAFYSEQPDFSGHKYGPFGPESSYSGSPPTPAKPRKRVAPKRRQRPVAPPKRRR 360
Db 301 PSVAFYSEQPDFSGHKYGPFGPESSYSGSPPTPAKPRKRVAPKRRQRPVAPPKRRR 360

QY 361 KIHMDHYAAETRODKMTNPLREIDKIVGQMDGLKQLKLRCCVNVIFVGDHGMEDVTCD 420
Db 361 KIHMDHYAAETRODKMTNPLREIDKIVGQMDGLKQLKLRCCVNVIFVGDHGMEDVTCD 420
QY 421 RTEFLSNLYTNVDDITLPGTGLRIRSFNSNAKYDPAKAIANLCKKPDQHFKPYLKQH 480
Db 421 RTEFLSNLYTNVDDITLPGTGLRIRSFNSNAKYDPAKAIANLCKKPDQHFKPYLKQH 480
QY 481 LPKRLHYANNRRIEDIHLLVRRHVARKPLDYKKPSGKCFQGDHGFDNKVNQMOTVF 540
Db 481 LPKRLHYANNRRIEDIHLLVRRHVARKPLDYKKPSGKCFQGDHGFDNKVNQMOTVF 540
QY 541 VGYGPTFKYTKVPPFENIELYNMCDLLGLKPAENNGTHGSLNHLRLTNTFRPTMPEV 600
Db 541 VGYGPTFKYTKVPPFENIELYNMCDLLGLKPAENNGTHGSLNHLRLTNTFRPTMPEV 600
QY 601 TRPNYPMYLSQDFDLGCTCDDKVEPKNKLDLNLKRLHGTSTGERHLLYGRPAVLYRT 660
Db 601 TRPNYPMYLSQDFDLGCTCDDKVEPKNKLDLNLKRLHGTSTGERHLLYGRPAVLYRT 660
QY 661 RYDILYHTDFESGYSEIFLMLLWTSYTSKQAEVSSVPDHLTSCVPRDVRVSPFSQNC 720
Db 661 RYDILYHTDFESGYSEIFLMLLWTSYTSKQAEVSSVPDHLTSCVPRDVRVSPFSQNC 720
QY 721 AYKNDKQMSYGLFPPYLSPPYSSPEAKYDAFLVTNMVPMYPAKRVWNYFORVLVKKYASER 780
Db 721 AYKNDKQMSYGLFPPYLSPPYSSPEAKYDAFLVTNMVPMYPAKRVWNYFORVLVKKYASER 780
QY 781 NGVNVISGPIFYDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGP 840
Db 781 NGVNVISGPIFYDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGP 840
QY 841 LSVSFFILPHRPNDESCNSEDSESKVVEELMKMHTARVROIEHLTSLDFFRKTSTRSYPE 900
Db 841 LSVSFFILPHRPNDESCNSEDSESKVVEELMKMHTARVROIEHLTSLDFFRKTSTRSYPE 900
QY 901 ILTLKTYLHYEISEI 915
Db 901 ILTLKTYLHYEISEI 915

RESULT 4
US-08-346-455B-34
; Sequence 34, Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORGAN & FINNEGAN
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346.455B
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 829
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Melanoma
CELL LINE: A2058
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: Putative protein
OTHER INFORMATION: sequence of A2058 Autotaxin
US-08-346-455B-34

Query Match 90.3%; Score 4533; DB 1; Length 829;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 87 CHDFDELCLKTARGWECTKDRGCEVRNEENACHSCSDCLARGDCCTNYOVVCKGESHVWD 146
Db 1 CHDFDELCLKTARGWECTKDRGCEVRNEENACHSCSDCLARGDCCTNYOVVCKGESHVWD 60
QY 147 DCCEEIKAAECAPAGFVRPPLIIFSVDFRASVMKSGKVMNPNIETKLRSCGTHSPYMRPVY 206
Db 61 DCCEEIKAAECAPAGFVRPPLIIFSVDFRASVMKSGKVMNPNIETKLRSCGTHSPYMRPVY 120
QY 207 PKTFNLYTLATGLYPESHGIVGNSMYDPVDFATPHLRGKREKFNHRWGGQPLWTATK 266
Db 121 PKTFNLYTLATGLYPESHGIVGNSMYDPVDFATPHLRGKREKFNHRWGGQPLWTATK 180
QY 267 QGVKAGTFEWSVVIPIHERRILTLRLWTLDPHERPSVAFYSEQPDFSGHKYGFPGPEES 326
Db 181 QGVKAGTFEWSVVIPIHERRILTLRLWTLDPHERPSVAFYSEQPDFSGHKYGFPGPEES 240
QY 327 SYGSPFTPAKRPKRKYAPKRRQERPVAPPKRRRKIRHMDHYAAETRODKMTNPLREIDK 386
Db 241 SYGSPFTPAKRPKRKYAPKRRQERPVAPPKRRRKIRHMDHYAAETRODKMTNPLREIDK 300
QY 387 IVGQLMDGLKQLKLRCCVNVIFVGDHGMEDVTCDRTEFLSNLYTNVDDITLPGTGLRIR 446
Db 301 IVGQLMDGLKQLKLRCCVNVIFVGDHGMEDVTCDRTEFLSNLYTNVDDITLPGTGLRIR 360
QY 447 SKFSNNAKYDPAKAIANLCKKPDQHFKPYLKQHLKPRLHYANNRRIEDIHLLVRRHV 506
Db 361 SKFSNNAKYDPAKAIANLCKKPDQHFKPYLKQHLKPRLHYANNRRIEDIHLLVRRHV 420
QY 507 ARKPLDYKKPSGKCFQGDHGFDNKVNQMOTVFVGYGPTFKYTKVPPENIELYNMVC 566
Db 507 ARKPLDYKKPSGKCFQGDHGFDNKVNQMOTVFVGYGPTFKYTKVPPENIELYNMVC 566

Db 421 ARKPLDVYKPSGKCFQGDHGFDNKVNMSQTVFVGYGTFKTKVPFENIELYNVMC 480
Qy 567 DLLGLKPAPNNGTHGSLNHLRTNFRPTMPEVTRPNYPGIMYLOSDFDLGCTCDDKVE 626
Db 481 DLLGLKPAPNNGTHGSLNHLRTNFRPTMPEVTRPNYPGIMYLOSDDDLGCTCDDKVE 540
Qy 627 PNKLDLNLKRLHTKSTGERHLLYGRPAVLYRTRDYDLYHTDFESGYSEIFLMLLWTSY 686
Db 541 PNKLDLNLKRLHTKSTGERHLLYGRPAVLYRTRDYDLYHTDFESGYSEIFLMLLWTSY 600
Qy 687 TVSKQAEVSSVPDHLTSCVRPDRVSPFSQNCCLAYKNDKQMSYGLFPFYLSSSPEAKY 746
Db 601 TVSKQAEVSSVPDHLTSCVRPDRVSPFSQNCCLAYKNDKQMSYGLFPFYLSSSPEAKY 660
Qy 747 DAFLVTNMPVMPYPAFKRVWNYFORVLVKKYASERGNVVISGPIFYDYDGLHDTEDKIK 806
Db 661 DAFLVTNMPVMPYPAFKRVWNYFORVLVKKYASERGNVVISGPIFYDYDGLHDTEDKIK 720
Qy 807 QYVEGSSIPVPHYSIITSCIDFTQPADKCDGPLSVSSFILPHRPDNEBSCNSESDESK 866
Db 721 QYVEGSSIPVPHYSIITSCIDFTQPADKCDGPLSVSSFILPHRPDNEBSCNSESDESK 780
Qy 867 WVEELMKMHTARVDIEHLTSLDFRKTSSRSYPEILTKTYLHTYESEI 915
Db 781 WVEELMKMHTARVDIEHLTSLDFRKTSSRSYPEILTKTYLHTYESEI 829

RESULT 5

US-08-977-221-34

; Sequence 34, Application us/08977221

; Patent No. 6084069

; GENERAL INFORMATION:

; APPLICANT: UNITED STATES OF AMERICA; DEPT.

; APPLICANT: OF HEALTH AND HUMAN SERVICES

; TITLE OF INVENTION: MOTILITY STIMULATING

; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND

; TITLE OF INVENTION: THERAPY

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN

; STREET: 345 PARK AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: U.S.A.

; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/977,221

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/346,455

; FILING DATE: 28-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/249,182

; FILING DATE: 25-MAY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/822,043

; FILING DATE: 17-JAN-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: DOROTHY R. AUTH

; REGISTRATION NUMBER: 36,434

; REFERENCE/DOCKET NUMBER: 2026-4149US3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 758-4800

; TELEFAX: (212) 751-6849

; INFORMATION FOR SEQ ID NO: 34:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 829

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Melanoma
; CELL LINE: A2058
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: Putative protein
; OTHER INFORMATION: sequence of A2058 Autotaxin
; US-08-977-221-34

Query Match 90.3%; Score 4533; DB 3; Length 829;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 828; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 87 CHDFDELCLKTARGWECTKDRGGEVRNEENACHSECLARGDCCTNYQVVKGESHWD 146
Db 1 CHDFDELCLKTARGWECTKDRGGEVRNEENACHSECLARGDCCTNYQVVKGESHWD 60
QY 147 DCCEETKAAECPCAGFVRPPLIIFSVDFRASYMKKSGKVMNIEKLSRSCGTHSPMRPVY 206
Db 61 DCCEETKAAECPCAGFVRPPLIIFSVDFRASYMKKSGKVMNIEKLSRSCGTHSPMRPVY 120
QY 207 PTTFPNLYTLATGLYPESHGIVGNSMYDPVDFATFHLRGREKFNHRWGGQPLWITATK 266
Db 121 PTTFPNLYTLATGLYPESHGIVGNSMYDPVDFATFHLRGREKFNHRWGGQPLWITATK 180
QY 267 QGVKAGTFFWSVIPHERRIITILRWLTLPDHERPSVAFYSEQDFSGHKYGFPGPEES 326
Db 181 QGVKAGTFFWSVIPHERRIITILRWLTLPDHERPSVAFYSEQDFSGHKYGFPGPEES 240
QY 327 SYGSPPTPAKRPRKRVAPKRQRPVAPPKRRRKIRHMDHYAAETRODKMTNPLREIDK 386
Db 241 SYGSPPTPAKRPRKRVAPKRQRPVAPPKRRRKIRHMDHYAAETRODKMTNPLREIDK 300
QY 387 IVGQMDGLKQLRRCVNVIFVGDHGMEDVTCORTFSLNLTNVDDITLVPGTLGRIR 446
Db 301 IVGQMDGLKQLRRCVNVIFVGDHGMEDVTCORTFSLNLTNVDDITLVPGTLGRIR 360
QY 447 SKFSNNAKYDPKAIANLTCKKPDQHEKPYLKQHLPRKRLHYANNRRRIEDIHLLVERRHV 506
Db 361 SKFSNNAKYDPKAIANLTCKKPDQHEKPYLKQHLPRKRLHYANNRRRIEDIHLLVERRHV 420
QY 507 ARKPLDVYKPSGKCFQGDHGFDNKVNMSQTVFVGYGTFKTKVPFENIELYNVMC 566
Db 421 ARKPLDVYKPSGKCFQGDHGFDNKVNMSQTVFVGYGTFKTKVPFENIELYNVMC 480
QY 567 DLLGLKPAPNNGTHGSLNHLRTNFRPTMPEVTRPNYPGIMYLOSDFDLGCTCDDKVE 626
Db 481 DLLGLKPAPNNGTHGSLNHLRTNFRPTMPEVTRPNYPGIMYLOSDDDLGCTCDDKVE 540
QY 627 PNKLDLNLKRLHTKSTGERHLLYGRPAVLYRTRDYDLYHTDFESGYSEIFLMLLWTSY 686
Db 541 PNKLDLNLKRLHTKSTGERHLLYGRPAVLYRTRDYDLYHTDFESGYSEIFLMLLWTSY 600
QY 687 TVSKQAEVSSVPDHLTSCVRPDRVSPFSQNCCLAYKNDKQMSYGLFPFYLSSSPEAKY 746
Db 601 TVSKQAEVSSVPDHLTSCVRPDRVSPFSQNCCLAYKNDKQMSYGLFPFYLSSSPEAKY 660
QY 747 DAFLVTNMPVMPYPAFKRVWNYFORVLVKKYASERGNVVISGPIFYDYDGLHDTEDKIK 806

Db 661 DAFLVTNMPYPAKRWNYFORVLVKYASRGNVVISGPIFDYDGLHDTEDKIK 720
QY 807 QYVGGSSIPVTHYYSITSLDFTQPADKCDGPLSVSFFILPHRPDNEESCNSSEDESK 866
Db 721 QYVGGSSIPVTHYYSITSLDFTQPADKCDGPLSVSFFILPHRPDNEESCNSSEDESK 780
QY 867 WVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLTKTYLHTYSEI 915
Db 781 WVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLTKTYLHTYSEI 829

RESULT 6
PCT-US95-06613-34
; Sequence 34, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 829
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHEetical: No
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Melanoma
; CELL LINE: A2058
; ORGANELLE:

; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: Putative protein
; OTHER INFORMATION: sequence of A2058 Autotaxin
PCT-US95-06613-34

Query Match 90.3%; Score 4533; DB 5; Length 829;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 87 CHDFDELCLKTARGWECTKDRGCEVRNEENACHSCSEDCLARGDCTNYQVVKGESHWVD 146
Db 1 CHDFDELCLKTARGWECTKDRGCEVRNEENACHSCSEDCLARGDCTNYQVVKGESHWVD 60
QY 147 DCEETKAAECAPAGFVRPPLIIFSVDFRASYMKKSKVMPNIEKLRSCGTHSPYMRPVY 206
Db 61 DCEETKAAECAPAGFVRPPLIIFSVDFRASYMKKSKVMPNIEKLRSCGTHSPYMRPVY 120
QY 207 PTKTFPNLYTLATGLYPESHGIVGNSMDPVDFATFHLRGREKFNHRWGGQPLWITATK 266
Db 121 PTKTFPNLYTLATGLYPESHGIVGNSMDPVDFATFHLRGREKFNHRWGGQPLWITATK 180
QY 267 QGVKAGTFEWSVVIPIHERILLITLRLWTLTPDHERPSVYAFYSEQPDFSGHKYGPFGPEES 326
Db 181 QGVKAGTFEWSVVIPIHERILLITLRLWTLTPDHERPSVYAFYSEQPDFSGHKYGPFGPEES 240
QY 327 SYGSPPTPAKRPRKRVAPKRQERPVAPKRRRKIHRMDHYAAETRODKMTNPLREIDK 386
Db 241 SYGSPPTPAKRPRKRVAPKRQERPVAPKRRRKIHRMDHYAAETRODKMTNPLREIDK 300
QY 387 IVGQMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGTLGRIR 446
Db 301 IVGQMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGTLGRIR 360
QY 447 SKFSNNAKYDPRKAIANLTKCKPDQHFKPYLKOHLPRKRLHYANNRRIEDIHLVERRWHV 506
Db 361 SKFSNNAKYDPRKAIANLTKCKPDQHFKPYLKOHLPRKRLHYANNRRIEDIHLVERRWHV 420
QY 507 ARKPLDYKKPSGKCFQGDHGDKNVNSMQTVFVGYPGTFKYTKVPPENIELYNVVC 566
Db 421 ARKPLDYKKPSGKCFQGDHGDKNVNSMQTVFVGYPGTFKYTKVPPENIELYNVVC 480
QY 567 DLGLKAPAPNNGTHGSLNHLRLTNTFRTPMPEEVRPNYPGIMYLOSDFDLGCTCDKVE 626
Db 481 DLGLKAPAPNNGTHGSLNHLRLTNTFRTPMPEEVRPNYPGIMYLOSDFDLGCTCDKVE 540
QY 627 PKNKLDLKNRLHTKSTGERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSY 686
Db 541 PKNKLDLKNRLHTKSTGERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSY 600
QY 687 TVSKQAEVSSVPDHLTSCVRPDRVRSFSPQCLAYKNDKQMSYGFLLFPYLSSSPEAKY 746
Db 601 TVSKQAEVSSVPDHLTSCVRPDRVRSFSPQCLAYKNDKQMSYGFLLFPYLSSSPEAKY 660
QY 747 DAFLVTNMPYPAKRWNYFORVLVKYASRGNVVISGPIFDYDGLHDTEDKIK 806
Db 661 DAFLVTNMPYPAKRWNYFORVLVKYASRGNVVISGPIFDYDGLHDTEDKIK 720
QY 807 QYVGGSSIPVTHYYSITSLDFTQPADKCDGPLSVSFFILPHRPDNEESCNSSEDESK 866
Db 721 QYVGGSSIPVTHYYSITSLDFTQPADKCDGPLSVSFFILPHRPDNEESCNSSEDESK 780
QY 867 WVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLTKTYLHTYSEI 915
Db 781 WVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLTKTYLHTYSEI 829

RESULT 7
US-08-346-455B-67
; Sequence 67, Application US/08346455B

Patent No. 5731167
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US/08/346,455B
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 861
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: N-tera 2D1 ATX protein
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:

Query Match 88.0%; Score 4418; DB 1; Length 861;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 822; Conservative 12; Mismatches 19; Indels 70; Gaps 6;
QY 1 MARRSFQSQIISLTFVAVGVCISLIGFTAHRIKRAEGWEGPPTVLSDSPWTNIGSGCK 60
DB 1 MARRSFQSQIISLTFVAVGVCISLIGFTAHRIKRAEGWEGPPTVLSDSPWTNIGSGCK 60
QY 61 GRCFELQAGPPDCRDNLCCKSTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC 120
DB 61 GRCFELQAGPPDCRDNLCCKSTSCCHDFDELCLKTARAWECTNDRCGEVRNEENACHC 120
QY 121 SEDCLARGDCCTNYQVVKGESHWDCCBEIKAAECPAGFVRPPLIIFSVYDGFRASTYMK 180
DB 121 SEDCLARGDCCTNYQVVKGESHWDCCBEIKAAECPAGFVRPPLIIFSVYDGFRASTYMK 180
QY 181 KGSKVPNIEKLRSCGTHSPMRPVYTKTFPNLYTLATGLYPESHGIVGNSMYDVPVDA 240

DB 181 KGSKVPNIEKLRSCGTHSPMRPVYTKTFPNLYTLATGLYPESHGIVGNSMYDVPVDA 240
QY 241 TTHLRGKREKFNHRWGGQPLWTATATKQGVKAGTFFWSVVI---PHERRLLTLRLWLTLP 296
DB 241 TTHLRGKREKFNHRWGGQPLWTATATKQGVKAGTFFWSVVI---PHERRLLTLRLWLTLP 296
QY 297 DHER-----PSVYAFYSEQPDFSGHKYGPFGPESSYSGSPPTPAKRPKRVAPKRRQERP 352
DB 297 DHERLRSMPFSLNL-----ISLDTNMPGPE----- 352
QY 353 APPKRRRRKIHRRMDHYAAETRODKMTNPLREIDKIYQQLMDGLKQLKLRVNVVIFGDH 412
DB 353 APPKRRRRKIHRRMDHYAAETRODKMTNPLREIDKIYQQLMDGLKQLKLRVNVVIFGDH 412
QY 413 GMEDVTCDRTEFLSNLYLTNVDDITLVPGLGRISFESNNAKYDPKAIANLCKKPDQH 472
DB 413 GMEDVTCDRTEFLSNLYLTNVDDITLVPGLGRISFESNNAKYDPKAIANLCKKPDQH 472
QY 472 FKPYLKQHLPLKRLHYANNRRIEDIHLVRRHWVARKPLDVKKPSGKCFQGDHGFNDK 532
DB 472 FKPYLKQHLPLKRLHYANNRRIEDIHLVRRHWVARKPLDVKKPSGKCFQGDHGFNDK 532
QY 533 VNSMOTVFGYGPFTFKYTKVPPFENIELYNVCMCDLLGLKPAENNGTHGSLNHLRTNF 592
DB 533 VNSMOTVFGYGPFTFKYTKVPPFENIELYNVCMCDLLGLKPAENNGTHGSLNHLRTNF 592
QY 593 RPTMPEEVRPNYPGIMYLOSDFDLGCTCDDKVEPKNKDELANKRLHTKGSTGERHLLYG 652
DB 593 RPTMPEEVRPNYPGIMYLOSDFDLGCTCDDKVEPKNKDELANKRLHTKGSTGERHLLYG 652
QY 653 RPAVLYTRYDILYHTDFESGYSEIFLMLLTWSTYVSKQAEVSSVPDHLTSCVRPDRVS 712
DB 653 RPAVLYTRYDILYHTDFESGYSEIFLMLLTWSTYVSKQAEVSSVPDHLTSCVRPDRVS 712
QY 713 PSFQNLAYKNDKQMSYGFLLPPLSSSPKAYDAFLVTNMVPMYPAKRVWNYQRVL 772
DB 713 PSFQNLAYKNDKQMSYGFLLPPLSSSPKAYDAFLVTNMVPMYPAKRVWNYQRVL 772
QY 773 VKKYASERNVNVISGPIFYDYDGLHDTEDKIKQVGEISSIPVPHYYSIITSCLDFTQ 832
DB 773 VKKYASERNVNVISGPIFYDYDGLHDTEDKIKQVGEISSIPVPHYYSIITSCLDFTQ 832
QY 833 PADKCDGPLSVSFFILPHRPDNEESCNSSEDSKWEELMKMHTARVRIEHLTSLDFFR 892
DB 833 PADKCDGPLSVSFFILPHRPDNEESCNSSEDSKWEELMKMHTARVRIEHLTSLDFFR 892
QY 893 KTSRSYPEILTLKTYLHTYSEI 915
DB 893 KTSRSYPEILTLKTYLHTYSEI 861

RESULT 8

US-08-977-221-67
Sequence 67, Application US/08977221
Patent No. 6084069
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible

REFERENCE/DOCKET NUMBER: 2026-4149US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 861
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: N-tera 2D1 ATX protein
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PCT-US95-06613-67

Query Match 88.0%; Score 4418; DB 5; Length 861;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 822; Conservative 12; Mismatches 19; Indels 70; Gaps 6;

Qy 1 MARRSFCQIISLFTFAVGSICLFTAHRIKRAEGWEEGPTVLSDSPWNTNIGSCK 60
Db 1 MARRSFCQIISLFTFAVGSICLFTAHRIKRAEGWEEGPTVLSDSPWNTNIGSCK 60
Qy 61 GRCFELQAGPPDCRDNLCYSCTCHDFDELCLKTARGWECTKRCGEVRNEENACHC 120
Db 61 GRCFELQAGPPDCRDNLCYSCTCHDFDELCLKTARGWECTKRCGEVRNEENACHC 120
Qy 121 SEDCLARGDCCTNYOVCKGESHVDDDCBEEIKAAECPCAGFVRPPLIIFSVDFRASVMK 180
Db 121 SEDCLARGDCCTNYOVCKGESHVDDDCBEEIKAAECPCAGFVRPPLIIFSVDFRASVMK 180
Qy 181 KGSVMNPTEKLRSGTSPYMRPVYPTKPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
Db 181 KGSVMNPTEKLRSGTSPYMRPVYPTKPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
Qy 241 TFHLRGREKHNRMWGGPPLWTATKQGVKAGTFEWSVVI-----PHERILTLRWLTLP 296
Db 241 TFHLRGREKHNRMWGGPPLWTATKQGVKAGTFEWSVVI-----PHERILTLRWLTLP 296
Qy 297 DHER-----PSVYAFYSEQDFSGHKYGPGEBSYSGSPFTPAKRKRKVPKRQRPV 352
Db 297 DHERLRSMPSILSNL-----ISLDTNMPGPE----- 323
Qy 353 APPKRRRKIHMDHYAAETROCKWTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDH 412
Db 324 -----MTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDH 359
Qy 413 GMEDVTCRTEFLSNLTVNDVITLVPGLGRIRSKFSNNAKYDPAKIIANTLTKKRPDQH 472
Db 360 GMEDVTCRTEFLSNLTVNDVITLVPGLGL-IRSKFSNNAKYDPAKIIANTLTKKRPDQH 418
Qy 473 FKPYLKQHLKRLHYANNRRIEDIHLLVERRWVHARKPLDYVKPSGKCFQGDHGFNDK 532
Db 419 FKPYLKQHLKRLHYANNRRIEDIHLLVERRWVHARKPLDYVKPSGKCFQGDHGFNDK 478
Qy 533 VNSQTVGVGPTPKYTKVPPFENIELYNVMDLLGLKAPNNGTHGSLNHLRTNTF 592
Db 479 VNSQTVGVGPTPKYTKVPPFENIELYNVMDLLGLKAPNNGTHGSLNHLRTNTF 538
Qy 593 RPTMPEEVRNYPGIMYQSDFDGCTCDDKVEPKNKLDELNKLRLHTKGSFEERHLLYG 652
Db 539 RPTMPEEVRNYPGIMYQSDFDGCTCDDKVEPKNKLDELNKLRLHTKGSFEERHLLYG 598
Qy 653 RPAVLYRTRDYLYHTDFESGYSEIFLMLLWTSYVSKQAEVSSVPDHLTSCVRPDPVRS 712
Db 599 RPAVLYRTRDYLYHTDFESGYSEIFLMLLWTSYVSKQAEVSSVPDHLTSCVRPDPVRS 658
Qy 713 PSFSONCLAYKNDKQMSYGFPPPYLSSSPEAKYDAFLVTNNMVPYPAFKRVNMFQFVL 772

Db 659 PSFSONCLAYKNDKQMSYGFPPPYLSSSPEAKYDAFLVTNNMVPYPAFKRVNMFQFVL 718
Qy 773 VKKYASERNGVNLSGRIFDYDYGDLHDTEDKIKQYVSGSSIPVPTHYYSIITSCLDFTQ 832
Db 719 VKKYASERNGVNLSGRIFDYDYGDLHDTEDKIKQYVSGSSIPVPTHYYSIITSCLDFTQ 778
Qy 833 PADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFR 892
Db 779 PADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFR 838
Qy 893 KTSRSYPEILTLKTYLHYESEI 915
Db 839 KTSRSYPEILTLKTYLHYESEI 861
RESULT 10
US-08-346-455B-38
; Sequence 38, Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,455B
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 979
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:

TISSUE TYPE: Liver
CELL TYPE:
CELL LINE:
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: putative autotaxin
OTHER INFORMATION: protein sequence from human liver
US-08-346-455B-38

Query Match 85.3%; Score 4279; DB 1; Length 979;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 805; Conservative 13; Mismatches 36; Indels 70; Gaps 8;

QY 1 MARRSFQSCQIISLFTFVAVGVSICLGFTHAIRKRAEGWEGPPTVLSDSPWNTISGCK 60
DB 1 MARRSFQSCQIISLFTFVAVGVSICLGFTHAIRKRAEGWEGPPTVLSDSPWNTISGCK 60
QY 61 GRCFELQAGPPDCRDNLCCKSYTSCCHDFDELCLKTARGWECTKDCRGEVRNENACHC 120
DB 61 GRCFELQAGPPDCRDNLCCKSYTSCCHDFDELCLKTARGWECTKDCRGEVRNENACHC 120
QY 121 SEDCLARGDCCTNYQVYCKGESHVWDDCEIEKAAECFAGFVRPPLIIIFSVDGF--RASY 178
DB 121 SEDCLARGDCCTNYQVYCKGESHVWDDCEIEKAAECFAGFVRPPLIIIFSVDGF--RASY 178
QY 179 MKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLPESHGIVGNSMYDVPF 238
DB 179 MKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLPESHGIVGNSMYDVPF 238
QY 239 DATFHLRGREKFNHRWGGOPLTATKQGVKAGTFWFSVVI---PHERILLTLRLWT 294
DB 239 DATFHLRGREKFNHRWGGOPLTATKQGVKAGTFWFSVVI---PHERILLTLRLWT 294
QY 295 LPDHERSVYAFYSEQDFSGHKYGPFGPESSYCGSPPTPAKRPRKRVAPRRQRVPAP 354
DB 295 LPDHERSVYAFYSEQDFSGHKYGPFGPESSYCGSPPTPAKRPRKRVAPRRQRVPAP 354
QY 355 PKRRRRKIRHMDHYAAETRODKMTPNREIDKIYQQLMDGLKQLKRCVNVFVGDHGM 414
DB 355 PKRRRRKIRHMDHYAAETRODKMTPNREIDKIYQQLMDGLKQLKRCVNVFVGDHGM 414
QY 415 EDVTC--RTEFLSNLYTNVDDITLVPGTLGRIBSKESNNAKYDPKAIANTCKKPDQH 472
DB 415 EDVTC--RTEFLSNLYTNVDDITLVPGTLGRIBSKESNNAKYDPKAIANTCKKPDQH 472
QY 473 FKPYLKQHLPKRLHYANNRRIEDIHLVERWHVARKPLDYVKKPSGKCFQGDHGFONK 532
DB 473 FKPYLKQHLPKRLHYANNRRIEDIHLVERWHVARKPLDYVKKPSGKCFQGDHGFONK 532
QY 533 VNSMQTVFVGYPGTFKYTKVPPFENIELYNVMDLLGLKAPNNGTHGSLNHLRLTNTF 592
DB 533 VNSMQTVFVGYPGTFKYTKVPPFENIELYNVMDLLGLKAPNNGTHGSLNHLRLTNTF 592
QY 593 RPTWPEVTRPNYPIGIMYLSQDFDGLCTCDKVPKKNLDELNKLRLHTKGSTEEHRLLYG 652
DB 593 RPTWPEVTRPNYPIGIMYLSQDFDGLCTCDKVPKKNLDELNKLRLHTKGSTEEHRLLYG 652
QY 653 -RPAVLYRTRDILYHDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVVRV 711
DB 653 -RPAVLYRTRDILYHDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVVRV 711
QY 712 SPFSQNLAYKNDKQMSYGLFPPYLSSSPEAKYDAFLVNMVPMYPAFKRVWNYFORV 771
DB 712 SPFSQNLAYKNDKQMSYGLFPPYLSSSPEAKYDAFLVNMVPMYPAFKRVWNYFORV 771
QY 772 LVKKYASERNVNSIGPIFYDYDGLHDTEDKIKQYVEGSSIPVPTHYIITSCLDFT 831
DB 772 LVKKYASERNVNSIGPIFYDYDGLHDTEDKIKQYVEGSSIPVPTHYIITSCLDFT 831

QY 832 OPADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFF 891
DB 780 OPADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFF 839
QY 892 RKTSRYPEILTKTYLHTYSEI 915
DB 840 RKTSRYPEILTKTYLHTYSEI 863
RESULT 11
US-08-977-221-38
; Sequence 38, Application US/08977221
; Patent No. 6084669
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-41490US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 979
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE: Liver
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:

IDENTIFICATION METHOD:
OTHER INFORMATION: putative autotaxin
OTHER INFORMATION: protein sequence from human liver
US-08-977-221-38

Query Match	85.3%;	Score 4279;	DB 3;	Length 979;	
Best Local Similarity	87.1%;	Pred. No. 0;			
Matches	805;	Conservative	13;	Mismatches	36;
				Indels	70;
				Gaps	8;
Qy	1	MARRSFQSCQIIISLFTAVGVISICLGFTHARIKRAEGWEEGPTVLSDSPTNISGSK	60		
Db	1	MARRSFQSCQDISLFTAVGVNICLGFTHARIKRAEGWEEGPTVLSDSPTNISGSK	60		
Qy	61	GRCELOAGPDDCDNLCKSYTSCCHDFDELCKLTARGWECTKRCGEVRNEENACHC	120		
Db	61	GRCELOAGPDDCDNLCKSYTSCCHDFDELCKLTARAWECTKRCGEVRNEENACHC	120		
Qy	121	SEDCIARGDCCTNYOVCKGESHVDDDCETKAAECPAGFVRPPLTIIFSVDGF--RAS	178		
Db	121	SEDCIARGDCCTNYOVCKGESHVDDDCETKAAECLQ--VCSPSINHLLRGWLPTSY	178		
Qy	179	MKGSKVMNIEKLRSCGTHSYMPRVPTKTFPNLYTLATGLYPESHGIVGNSMYDPVF	238		
Db	179	MKGSKVMNIEKLRSCGTHSYMPRVPTKTFPNLYTLATGLYPESHGIVGNSMYDPVF	238		
Qy	239	DATHLRGREKFNHWGQPLWITATKQGVKAGTFEWSVVI----PHERRILITLRWLT	294		
Db	239	DATHLRGREKFNHWGQPLWITATKORGES----WNILLVCCHPRAEILITLQWLT	294		
Qy	295	LPDHERPSVYAFYSQDPFSGHKYGFPGPESSYSGPTPAKRPRKRVAKPRRQRPVAP	354		
Db	295	LPDHERPSVYAFYSQDPFSGHKHMPGPE-----	324		
Qy	355	PKRRRRKTHRMDHYAAETRQDKMTNPLREIDKIVQQLMDGLKQLKLRVCNVVIFVGDHGM	414		
Db	325	-----MTNPLREMHKIVGQMDGLKQLKLRVCNVVIFV---ET	359		
Qy	415	EDVTCD--RTFELSNTLVNDITLVPGLGRIRKFSNNAYDKPAITANLTCKKPDQH	472		
Db	360	MDGRCHMYRTFELSNTLVNDITLVPGLGRIRKFSNNAYDKPAITANLTCKKPDQH	419		
Qy	473	FKPYLQHLKRLHYANNRRITIEDHLLVERHWVARKPLDVYKKGSGKCFQGDHGFNDK	532		
Db	420	FKPYLQHLKRLHYANNRRITIEDHLLVERHWVARKPLDVYKKGSGAFSRETTAFDNR	479		
Qy	533	VNSQTVFVGYPGTFKYYTKVPPFENIELYNVCMCDLGLKPAPNNGTHGSLNHLRTNFF	592		
Db	480	VNSQTVFVGYPGTFKYYTKVPPFENIELYNVCMCDLGLKPAPNNGTHGSLNHLRTNFF	539		
Qy	593	RPTWPEEVRPNYQIMYLSQSDFLGCTCDDKVEPKNLDELNKLHRTKGSFEERHLLYG	652		
Db	540	RPTWPEEVRPNYQIMYLSQSDFLGCTCDDKVEPKNLDELNKLHRTKGSFEERHLLYG	599		
Qy	653	-RPAVLRYTRDILYHTDFESYSEIFLMLWTSYTVSKQAEVSSVPDHLTSCVRPDVRV	711		
Db	600	DRPAVLRYTRDILYHTDFESYSEIFLMLWTSYTVSKQAEVSSVPDHLTSCVRPDVRV	659		
Qy	712	SPFSQNCIAYKNDKQMSYGLFPPYLSSSPEAKYDAFLVTNNVPMYPAFKRWNYFORV	771		
Db	660	SPFSQNCIAYKNDKQMSYGLFPPYLSSSPEAKYDAFLVTNNVPMYPAFKRWNYFORV	719		
Qy	772	LVKKYASERNGVNISGPIFYDYDGLDHTEDKIQYVEGSSIPVPTHYYSITSCLDFT	831		
Db	720	LVKKYASERNGVNISGPIFYDYDGLDHTEDKIQYVEGSSIPVPTHYYSITSCLDFT	779		
Qy	832	QPADKCDGPLSVSSFILPHRPDNEESCNSSDESKWVEELMKMHTARVARDIEHLTSLDFF	891		
Db	780	QPADKCDGPLSVSSFILPHRPDNEESCNSSDESKWVEELMKMHTARVARDIEHLTSLDFF	839		
Qy	892	RKTSRSPYEILTLKTYLHYESEI	915		
Db	840	RKTSRSPYEILTLKTYLHYESEI	863		

RESULT 12
PCT-US95-06613-38
Sequence 38, Application PC/TUS95056613
GENERAL INFORMATION:
APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
APPLICANT: HENRY; MURATA, JUN
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 979
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE: Liver
CELL TYPE:
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: putative autotaxin
OTHER INFORMATION: protein sequence from human liver
PCT-US95-06613-38

Best Local Similarity 87.1%; Pred. No. 0; Mismatches 13; Gaps 8;
Matches 805; Conservative 36; Indels 70; Gaps 8;
QY 1 MARRSSFQSCQIISLTFEAVGSGICLGFTHRIKRAEGWEEGPTVLSDSPWNTNIGSCK 60
Db 1 MARRSSFQSCQIISLTFEAVGSGICLGFTHRIKRAEGWEEGPTVLSDSPWNTNIGSCK 60
QY 61 GRCFELQEAQPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDCRGGEVRNEENACHC 120
Db 61 GRCFELQEAQPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDCRGGEVRNEENACHC 120
QY 121 SEDCLARGDCCTNYQVCKGESHWDDCEIEKAAECFAGFVRPPLIFSDGDF--RASV 178
Db 121 SEDCLARGDCCTNYQVCKGESHWDDCEIEKAAECFAGFVRPPLIFSDGDF--RASV 178
QY 179 MKGSKVMPNIEKLRSGTHSPYMRPVYPTKTPNLTATGLYPESHGIVGNSMYDPVF 238
Db 179 MKGSKVMPNIEKLRSGTHSPYMRPVYPTKTPNLTATGLYPESHGIVGNSMYDPVF 238
QY 239 DATFHLRGREKFNHRWGGQPLMITATKQGVKAGTFWFSVVI-----PHERRILTLRLWT 294
Db 239 DATFHLRGREKFNHRWGGQPLMITATKQGVKAGTFWFSVVI-----PHERRILTLRLWT 294
QY 295 LPDHERPSVYAFYSEQDFSGHYKPGPPESSYSGSFTPAKRPKRKVAPKRRORPVP 354
Db 295 LPDHERPSVYAFYSEQDFSGHYKPGPPESSYSGSFTPAKRPKRKVAPKRRORPVP 354
QY 355 PKRRRRIHRMDHYAAETRODKWNTNPLRETDKIVGQMDGLKQLKLRRCVNVIFVGDHGM 414
Db 355 PKRRRRIHRMDHYAAETRODKWNTNPLRETDKIVGQMDGLKQLKLRRCVNVIFVGDHGM 414
QY 415 EDVTC--RTEFSLNLTNVDITLVPGLGRIRSKFSNNAKYDPKAIANLTCKKPDQH 472
Db 415 EDVTC--RTEFSLNLTNVDITLVPGLGRIRSKFSNNAKYDPKAIANLTCKKPDQH 472
QY 473 FKPYLQHLKRLHYANNRRIEDIHLLVERHWVARKPLDVYKPKSCKCFQGDHGFQDNK 532
Db 473 FKPYLQHLKRLHYANNRRIEDIHLLVERHWVARKPLDVYKPKSCKCFQGDHGFQDNK 532
QY 533 VNSMOTVFGYGTGPKYKTKVPPENIELYNVMDLLGLKLPAPNNGTHGSNLHLRTNTE 592
Db 533 VNSMOTVFGYGTGPKYKTKVPPENIELYNVMDLLGLKLPAPNNGTHGSNLHLRTNTE 592
QY 593 RPTMPEVTRPNYPGIMYLOSDFGLGCTDDKVEPKNKLDLNLKRLHTKGSTEERHLLYG 652
Db 593 RPTMPEVTRPNYPGIMYLOSDFGLGCTDDKVEPKNKLDLNLKRLHTKGSTEERHLLYG 652
QY 653 -RPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDRV 711
Db 653 -RPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDRV 711
QY 712 SPFSQNLAYKNDKQMSYGLFPYLLSSSPEAKYDAFLTNMVPMPYPAFKRVNMYFORV 771
Db 712 SPFSQNLAYKNDKQMSYGLFPYLLSSSPEAKYDAFLTNMVPMPYPAFKRVNMYFORV 771
QY 772 LVKKYASERNVNVISGPIFDYDGLHEDTKIKQYVEGSSIPVTHYSIITSCLDFT 831
Db 772 LVKKYASERNVNVISGPIFDYDGLHEDTKIKQYVEGSSIPVTHYSIITSCLDFT 831
QY 832 QPADKCDGPLSVSSFILPHRPDNEESCNSSDESKWVEELMKMHTARVRDIEHLTSLDFF 891
Db 832 QPADKCDGPLSVSSFILPHRPDNEESCNSSDESKWVEELMKMHTARVRDIEHLTSLDFF 891
QY 892 RKTSSRSYPEILTLKTYLHYESEI 915
Db 892 RKTSSRSYPEILTLKTYLHYESEI 915
QY 840 RKTSSRSYPEILTLKTYLHYESEI 863
Db 840 RKTSSRSYPEILTLKTYLHYESEI 863

RESULT 13
US-08-346-455B-36
; Sequence 36, Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:

APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 788
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: No
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE: teratocarcinoma
CELL TYPE: N-tera 2D1
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: N-tera 2D1 putative
OTHER INFORMATION: ATX protein sequence
US-08-346-455B-36

Query Match . 76.5%; Score 3842; DB 1; Length 788;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 727; Conservative 12; Mismatches 40; Indels 70; Gaps 8;

QY 76 CDNLCKSYTSCCHDFDELCLKTARGWECTKDCRGGEVRNEENACHCSEDCLARGDCCTNYQ 135
Db 1 CDNLCKSYTSCCHDFDELCLKTARGWECTKDCRGGEVRNEENACHCSEDCLARGDCCTNYQ 60

QY 136 VVKGESHWDDDCCEIKAAECAPAGVRPPLIIFSVDFG--RASVMKKGSKVMPNIEKLR 193
DB 61 VVKGESHWDDDCCEIKAAECQ--VDSPSINHLLRGWLPMTSYMKKGSKVMPNIEKLR 118
QY 194 SCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMDVPDFATFHLRGREKFNHR 253
DB 119 SCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMDVPDFATFHLRGREKFNHR 178
QY 254 WVGQPLWITATKQGVKAGTFWFSVVI---PHERILTLRLWTLPLDHERPSVYAFYSE 309
DB 179 WVGQPLWITATKQGES-----WNILLVCHPSRAELTLQWLTLPLDHERPSVYAFYSE 234
QY 310 QDFSGHKYGPFGPESSYSGSPETPAKREKRVAPKRRQERPVPAPKRRKRIHRMDHYA 369
DB 235 QDFSGHKHMPGPE----- 249
QY 370 AETRODKMTNPLREIDKIVGQMDGLKQLKLRVNVIFVGDHGMEDVTC--RTEFLSN 427
DB 250 -----MPNPLREMHKIVGQMDGLKQLKLRVNVIFV---ETMDGRCHMYRTEFLSN 299
QY 428 YLTNVDDITLVPGTGLGRISKFSNNAKYDPKAIANLTCKKPDQHFEPYKQLHLPKRLHY 487
DB 300 YLTNVDDITLVPGTGLGRISKFSNNAKYDPKAIANLTCKKPDQHFEPYKQLHLPKRLHY 359
QY 488 ANNRIEDIHLVERHWHVARKPLDYVKKPSGKCFQGDHGFNDKYNMOTVFGVGYGPTF 547
DB 360 ANNRIEDIHLVERHWHVARKPLDYVKKPSGNAFSRETTAFDNKYNMOTVFGVGYGPTF 419
QY 548 KYTKVPPFENIELYNVMDLGLKLPAPNNGTHGSLNHLRTNTFRPTMPEEYTRPNYPG 607
DB 420 KYTKVPPFENIELYNVMDLGLKLPAPNNGTHFSLNHLRTNTFRPTMPEEYTRPNYPG 479
QY 608 IMYLSQDFDLGCTCDKVPKKNKLDLNLKRLTKGSTEERHLLYG--RPVLYTRTDILY 666
DB 480 IMYLSQDFDLGCTCDKVPKKNKLDLNLKRLTKGSTEERHLLYGDRPAVLYTRYDILY 539
QY 667 HDFSFGYSEIFLMLLWTSYVSKQAEVSVDPDLTSCVRPDRVSPFSQNCGLAYKNDK 726
DB 540 HDFSFGYSEIFLMLWTSYVSKQAEVSVDPDLTSCVRPDRVSPFSQNCGLAYKNDK 599
QY 727 QMSYGLFPPYLLSSPEAKYDAFLVTNMPYPAFRVWNYFORVLVKKYASERNGVNI 786
DB 600 QMSYGLGPPYLLSSPEAKYDAFLVTNMPYPAFRVWNYFORVLVKKYASERNGVNI 659
QY 787 SGPIFDYDGLHDTEDTKIQVVEGSSIPVPHYYSIITSCLDFTQPAKCDGPLSVSSF 846
DB 660 SGPIFDYDGLHDTEDTKIQVVEGSSIPVPHYYSIITSCLDFTQPAKCDGPLSVSSF 719
QY 847 ILPHRPDNEESCSNDESKWVEELMKMTARVDRDIEHLTSLDFFRKTSSYPEILTLKT 906
DB 720 ILPHRPDNEESCSNDESKWVEELMKMTARVDRDIEHLTSLDFFRKTSSYPEILTLKT 779
QY 907 YLHTYESEI 915
DB 780 YLHTYESEI 788
RESULT 14
US-08-977-221-36
; Sequence 36, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK

COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,221
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 788
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: No
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: teratocarcinoma
CELL LINE: N-tera 2D1
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: N-tera 2D1 putative
OTHER INFORMATION: ATX protein sequence
US-08-977-221-36

Query Match 76.5%; Score 3842; DB 3; Length 788;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 727; Conservative 12; Mismatches 40; Indels 70; Gaps 8;

QY 76 CDNLCKSVTSCCHDFDELCLKTARGWECTKRCGEVRNEENACHSCDCLARGDCCTNYQ 135
DB 1 CDNLCKSVTSCCHDFDELCLKTARGWECTKRCGEVRNEENACHSCDCLARGDCCTNYQ 60
QY 136 VVKGESHWDDDCCEIKAAECAPAGVRPPLIIFSVDFG--RASVMKKGSKVMPNIEKLR 193
DB 61 VVKGESHWDDDCCEIKAAECQ--VDSPSINHLLRGWLPMTSYMKKGSKVMPNIEKLR 118
QY 194 SCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMDVPDFATFHLRGREKFNHR 253
DB 119 SCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMDVPDFATFHLRGREKFNHR 178
QY 254 WVGQPLWITATKQGVKAGTFWFSVVI---PHERILTLRLWTLPLDHERPSVYAFYSE 309
DB 179 WVGQPLWITATKQGES-----WNILLVCHPSRAELTLQWLTLPLDHERPSVYAFYSE 234

QY 310 QPDFSGHKYGPFGPESSYSGFPTPAKRPKRKVPAPKRRQERVPAPPKRRKKIHRMDHYA 369
| | | | | : | | | | |
Db 235 QPDFSGHKHMPGPE----- 249

QY 370 AETQDKMTPLREIDKIVGOLMDGLKLRRCVNVIFVGDHGMEDVTC--RTEFLSN 427
| | | | | : | | | | |
Db 250 -----MPNPLREMHKIVGOLMDGLKLRHRCVNVIFV---ETMDGRCHMYRTEFLSN 299
| | | | | : | | | | |
QY 428 YLTNVDDITLVPGLGRIRSFNSNAKVDPAKAIANLCKPKDQHFYKPKYKQHLPKRLHY 487
| | | | | : | | | | |
Db 300 YLTNVDDITLVPGLGRIRSFNSNAKVDPAKAIANLCKPKDQHFYKPKYKQHLPKRLHY 359
| | | | | : | | | | |
QY 488 ANNRRIEDIHLLVRRHVARPLDVYKPKSGKCFQGDHGFNDKVNMQTVFVGYGPTF 547
| | | | | : | | | | |
Db 360 ANNRRIEDIHLLVRRHVARPLDVYKPKSGNAPSRFTTAFDNKVNMQTVFVGYGPTF 419
| | | | | : | | | | |
QY 548 KYTKVPPFENIELYNVMDLLGLKPAFNGTHGSLNHLRLTNTFRPTMPEVTRPNYPG 607
| | | | | : | | | | |
Db 420 KYTKVPPFENIELYNVMDLLGLKPAFNGTHGSLNHLRLTNTFRPTMPEVTRPNYPG 479
| | | | | : | | | | |
QY 608 IMYLSQDFDLGCTCDDKVPKPKDELNKLRLTKGSTERHLLYG-RPVLVRYTRIDILY 666
| | | | | : | | | | |
Db 480 IMYLSQDFDLGCTCDDKVPKPKDELNKLRLTKGSTERHLLYGDRPAVLYTRIDILY 539
| | | | | : | | | | |
QY 667 HTDFESGYSEIFLMLLWTSYVSKQAEVSSVPDHLTSCVRPDVRSVPSFQNCCLAYKNDK 726
| | | | | : | | | | |
Db 540 HTDFESGYSEIFLMLWTSYVSKQAEVSSVPDHLTSCVRPDVRSVPSFQNCCLAYKNDK 599
| | | | | : | | | | |
QY 727 QMSYGFLLPPLSSSPEAKYDAFLVNMVPMYPAKRVNMVYQFVRLVKKYASERNGVNI 786
| | | | | : | | | | |
Db 600 QMSYGLGPPYLLSSSPEAKYDAFLVNMVPMYPAKRVNMVYQFVRLVKKYASERNGVNI 659
| | | | | : | | | | |
QY 787 SGPIFDYDGLHDTEDKIKQYVEGSSIPVTHYYSIITSCLDFTQPADKCDGPLSVSSF 846
| | | | | : | | | | |
Db 660 SGPIFDYDGLHDTEDKIKQYVEGSSIPVTHYYSIITSCLDFTQPADKCDGPLSVSSF 719
| | | | | : | | | | |
QY 847 ILPHRPNEESCNESEDESKVVEELMKMHTARVROIEHLTSLDFFRKTSRSPYELLTLTK 906
| | | | | : | | | | |
Db 720 ILPHRPNEESCNESEDESKVVEELMKMHTARVROIEHLTSLDFFRKTSRSPYELLTLTK 779
| | | | | : | | | | |
QY 907 YLHTYSEI 915
| | | | | : | | | | |
Db 780 YLHTYSEI 788
| | | | | : | | | | |

RESULT 15
PCT-US95-06613-36
; Sequence 36, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRI; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 788
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: No
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: teratocarcinoma
; CELL LINE: N-tera 2D1
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: N-tera 2D1 putative
; OTHER INFORMATION: ATX protein sequence
; PCT-US95-06613-36

Query Match 76.5%; Score 3842; DB 5; Length 788;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 727; Conservative 12; Mismatches 40; Indels 70; Gaps 8;

QY 76 CQNLKSYTSCCHDFDELCLKTARGWECTKDRGGEVNEENACHSEDCLARGDCCTNYQ 135
| | | | | : | | | | |
Db 1 CQNLKSYTSCCHDFDELCLKTARGWECTKDRGGEVNEENACHSEDCLARGDCCTNYQ 60
| | | | | : | | | | |
QY 136 VVCKGSHWVDDDCBEIKAAECFAGFVRPPLIIFSVDFG--RASVMKKGSKVMPNIEKLR 193
| | | | | : | | | | |
Db 61 VVCKGSHWVDDDCBEIKAAECFAGFVRPPLIIFSVDFG--RASVMKKGSKVMPNIEKLR 118
| | | | | : | | | | |
QY 194 SCGTHSPYRVPVPTKTFPNLYLATGLYPESHGIVGNSMYDPVDFATFHLRGKEFNHR 253
| | | | | : | | | | |
Db 119 SCGTHSPYRVPVPTKTFPNLYLATGLYPESHGIVGNSMYDPVDFATFHLRGKEFNHR 178
| | | | | : | | | | |
QY 254 WNGGQPLWITATKQYKAGTFFWSVVI-----PHERRILTILRLWTLTLPDHERPSVYAFSE 309
| | | | | : | | | | |
Db 179 WNGGQPLWITATKQYKAGTFFWSVVI-----PHERRILTILRLWTLTLPDHERPSVYAFSE 234
| | | | | : | | | | |
QY 310 QPDFSGHKYGPFGPESSYSGFPTPAKRPKRKVPAPKRRQERVPAPPKRRKKIHRMDHYA 369
| | | | | : | | | | |
Db 235 QPDFSGHKHMPGPE----- 249
| | | | | : | | | | |
QY 370 AETQDKMTNPLREIDKIVGOLMDGLKLRRCVNVIFVGDHGMEDVTC--RTEFLSN 427
| | | | | : | | | | |
Db 250 -----MPNPLREMHKIVGOLMDGLKLRHRCVNVIFV---ETMDGRCHMYRTEFLSN 299
| | | | | : | | | | |
QY 428 YLTNVDDITLVPGLGRIRSFNSNAKVDPAKAIANLCKPKDQHFYKPKYKQHLPKRLHY 487
| | | | | : | | | | |

Db	300	YLTNVDDITLVPGTIGRIRSFNSNAKVDPKAIIANLCTCKKPDQHFKPYLKQHLPRKLHY	359
Qy	488	ANNRIEDIHLIVERRRWHVARKPLDVIYKKPSGKCFQGDHGFNDKNVNSMOTVFVGYPTE	547
Db	360	ANNRIEDIHLIVERRRWHVARKPLDVIYKKPSGNAFSRETTAFDNKNVNSMOTVFVGYPTE	419
Qy	548	KYKTKVPPFENIELYNVCMDDLGLKPAHPNNGTHGSLNHLRTNTFRPTMPEEVTREPNYPG	607
Db	420	KYKTKVPPFENIELYNVCMDDLGLKPAHPNNGTHGSLNHLRTNTFRPTMPEEVTREPNYPG	479
Qy	608	IMYLOSDFDLGCTCDDKVEPKNKLDLKNKRLHTKGSTEERHLLYG-RPAVLYRTRYDILY	666
Db	480	IMYLOSDFDLGCTCDDKVEPKNKLDLKNKRLHTKGSTEERHLLYGDRPAVLYRTRYDILY	539
Qy	667	HTDFESGYSEIFLMLWTSYTVSKQAEVSSVPDHLTSCVRPDVRVSPSONCLAYKNDK	726
Db	540	HTDFESGYSEIFLMLWTSYTVSKQAEVSSVPDHLTSCVRPDVRVSPSONCLAYKNDK	599
Qy	727	QMSYGFLEPPPYLSSSPEAKYDAFLVTNMVPMYPAFKRVWNYFORVLVKKYASERNGVNVI	786
Db	600	QMSYGFLEPPPYLSSSPEAKYDAFLVTNMVPMYPAFKRVWNYFORVLVKKYASERNGVNVI	659
Qy	787	SGPIFDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSF	846
Db	660	SGPIFDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSF	719
Qy	847	ILPHRPDNEESCNSSEDESKWVEELMKMHTARVRODIEHLTSLDFFFKTSRSYPEILTLKT	906
Db	720	ILPHRPDNEESCNSSEDESKWVEELMKMHTARVRODIEHLTSLDFFFKTSRSYPEILTLKT	779
Qy	907	YLTHTYSEI 915	
Db	780	YLTHTYSEI 788	

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:43:22 ; Search time 25.97 Seconds
(without alignments)
2683.855 Million cell updates/sec

Title: US-09-483-831-69
Perfect score: 5019
Sequence: 1 MARRSFQSCQIISLFTFAV.....RSVPEILTKLTVLHYESEI 915

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	5019	100.0	915	A55144	autotaxin precursor
2	4306	85.8	885	A55453	plasma cell membra
3	2084	41.5	875	A57080	cell surface antig
4	1955.5	39.0	925	A39216	plasma cell membra
5	1899.5	37.8	905	A27410	plasma cell membra
6	646.5	12.9	457	T09932	nucleotide pyropho
7	612	12.2	496	T09931	nucleotide pyropho
8	611.5	12.2	479	T03293	nucleotide pyropho
9	610	12.2	829	T19494	hypothetical prote
10	609	12.1	451	T09933	nucleotide pyropho
11	539.5	10.7	485	T40857	probable phosphodie
12	522	10.4	429	T33724	hypothetical prote
13	461	9.2	433	B82537	phosphodiesterase-
14	456.5	9.1	674	T19495	hypothetical prote
15	456	9.1	300	A41179	protein kinase PC-
16	410	8.2	743	S19437	hypothetical prote
17	335.5	6.7	493	S50443	hypothetical prote
18	297.5	5.9	614	T30973	hypothetical prote
19	241.5	4.8	133	T09934	hypothetical prote
20	238	4.7	96	A25274	phosphodiesterase
21	238	4.7	453	T16795	hypothetical prote
22	163	3.2	360	T20867	hypothetical prote
23	146.5	2.9	329	NCBN1	nuclease NUC1 (EC
24	145.5	2.9	465	T34936	hypothetical prote
25	142	2.8	1186	T03180	tyrosine protein k
26	132	2.6	462	T36185	hypothetical prote
27	127	2.5	1820	A55494	latent transformin
28	123.5	2.5	454	A46498	glucocorticoid-sen
29	122	2.4	1374	S70712	protein-tyrosine k

30	121.5	2.4	2471	2	T03820	probable histidine
31	121	2.4	1888	2	T39009	hypothetical prote
32	119.5	2.4	475	2	A38340	66K glycoprotein p
33	119	2.4	2019	1	J01322	tenascin precursor
34	117	2.3	335	2	T11588	nuclease NUC1 (EC
35	116.5	2.3	989	2	S69711	hypothetical prote
36	112	2.2	1035	2	S61342	sulfite reductase
37	112	2.2	1394	2	A35626	transforming growt
38	112	2.2	2911	2	T20566	hypothetical prote
39	111	2.2	1394	2	A29637	position-specific
40	111	2.2	3002	2	A47221	fibrillin 1 precur
41	110.5	2.2	2871	2	A55567	fibrillin I - bovi
42	110.5	2.2	3147	2	T18674	hypothetical prote
43	110	2.2	753	2	T28787	hypothetical prote
44	109.5	2.2	476	1	SGMSV	vitronectin precur
45	109.5	2.2	1472	2	S67195	probable membrane

ALIGNMENTS

RESULT 1
A55144
autotaxin precursor - human
N:Contains: phosphodiesterase I (EC 3.1.4.1)
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A55144; A42329
J:Murata, J.; Lee, H.Y.; Clair, T.; Krutzsch, H.C.; Arestad, A.A.; Sobel, M.E.; Liott
J. Biol. Chem. 269, 30479-30484, 1994
A:Title: cDNA cloning of the human tumor motility-stimulating protein, autotaxin, rev
A:Reference number: A55144; MUID:95074054
A:Accession: A55144
A:Molecule type: mRNA
A:Residues: 1-915 <MUR>
A:CROSS-references: GB:L35594; NID:G537905; PIDN:AAA64785.1; PID:G537906
A:Note: parts of this sequence were confirmed by peptide sequencing
R:Stracke, M.L.; Krutzsch, H.C.; Unsworth, E.J.; Arestad, A.; Cioce, V.; Schiffmann,
J. Biol. Chem. 267, 2524-2529, 1992
A:Title: Identification, purification, and partial sequence analysis of autotaxin, a
A:Reference number: A42329; MUID:92129337
A:Accession: A42329
A:Molecule type: protein
A:Residues: 256-266;422-444;504-507,'AN';510,'X';511-515;533-548;'S',554-559,'N',561-
A:Experimental source: A2058 melanoma cells
A:Note: sequence extracted from NCBI backbone (NCBIP:78526, NCBIP:78523, NCBIP:78521,
A:Note: a peptide fragment Tyr-Asp-Val-Pro-Trp-Asp-Glu-Thr-Ile was also found
C:Comment: This protein acts as an autocrine factor to stimulate tumor cell motility.
C:Genetics:
A:Gene: GDB:ATX
A:CROSS-references: GDB:378346
A:Map position: 8q22-8qter
C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C:Keywords: EF hand; glycoprotein; phosphoric diester hydrolase
F:55-98/Domain: somatomedin B homology <SBH1>
F:99-142/Domain: somatomedin B homology <SBH2>
F:54,463,577,859/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:210/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 100.0%; Score 5019; DB 1; Length 915;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MARRSFQSCQIISLFTFAVGSICLGFTHRIKRAEGWEEGPTVLSDSPWNTNIGSSCK	60
Db	1	MARRSFQSCQIISLFTFAVGSICLGFTHRIKRAEGWEEGPTVLSDSPWNTNIGSSCK	60
Qy	61	GRCFEQLQAGPPDCRCDNLCKSYTSCCHDFDELCITARGWECTKRCGEVRNEENACHC	120
Db	61	GRCFEQLQAGPPDCRCDNLCKSYTSCCHDFDELCITARGWECTKRCGEVRNEENACHC	120
Qy	121	SEDCIARGDCCTNYQVVKGESHVWDDDCETKAAECAGFVRPLLIIFSVDFGRASYMK	180

Db 121 SECLARGDCCTNYQVVKGESHVDDCEIEIAAECPAGFVRPPLIFSVGDFRASYMK 180
QY 181 KGSVWPNIEKLSCGTHSPYMRVYTKFPNLYTLATGLYPESHGIVGSMYDPVEDA 240
Db 181 KGSVWPNIEKLSCGTHSPYMRVYTKFPNLYTLATGLYPESHGIVGSMYDPVEDA 240
QY 241 TFLHGREKENHNRWGGQPLWITATKGVAGTFFWVVIPIHERRILTLRLWILPDHER 300
Db 241 TFLHGREKENHNRWGGQPLWITATKGVAGTFFWVVIPIHERRILTLRLWILPDHER 300
QY 301 PSVYAFYSEQDFSGHKYGFPGPPESSYSGPFPAPKRPKRVAPKRRQERVPAPPKRRR 360
Db 301 PSVYAFYSEQDFSGHKYGFPGPPESSYSGPFPAPKRPKRVAPKRRQERVPAPPKRRR 360
QY 361 KIIRMDHYAAETRODKMTNPLREIDKIVGQMLGKQLKLRRCVNVIPVGDHGEDVTCD 420
Db 361 KIIRMDHYAAETRODKMTNPLREIDKIVGQMLGKQLKLRRCVNVIPVGDHGEDVTCD 420
QY 421 RTEFLSNLTNVDDITLVPGLTGRIRKFSNNAKYDPKAIITANLTCKPDQHFYKPKQH 480
Db 421 RTEFLSNLTNVDDITLVPGLTGRIRKFSNNAKYDPKAIITANLTCKPDQHFYKPKQH 480
QY 481 LPKRLHYANNRRIEDIHLVRRWHVARKPLDVYKPKSGKCFQGDHGFKNVNSMQTVF 540
Db 481 LPKRLHYANNRRIEDIHLVRRWHVARKPLDVYKPKSGKCFQGDHGFKNVNSMQTVF 540
QY 541 VGGPTFKYTKVPPFENIELYNVWCDLGLKLPAPNNGTHGSLNHLRTNFRPTMPREV 600
Db 541 VGGPTFKYTKVPPFENIELYNVWCDLGLKLPAPNNGTHGSLNHLRTNFRPTMPREV 600
QY 601 TRPNYPCIMTLQSDFDLGCTCDDKVEPKNLDELKRLHTKGTSEERHLLXGRPAVLRT 660
Db 601 TRPNYPCIMTLQSDFDLGCTCDDKVEPKNLDELKRLHTKGTSEERHLLXGRPAVLRT 660
QY 661 RYDILYHTDFESGYSEIFLMLLTSTYVSKQAEVSSVPDHLTSCVRPDRVYSPFSQNC 720
Db 661 RYDILYHTDFESGYSEIFLMLLTSTYVSKQAEVSSVPDHLTSCVRPDRVYSPFSQNC 720
QY 721 AYNDKQMSYGFLLPPLYLSSSPEAKYDAFLVNNVMPYPAKRVWNYQFQVLVKKYASER 780
Db 721 AYNDKQMSYGFLLPPLYLSSSPEAKYDAFLVNNVMPYPAKRVWNYQFQVLVKKYASER 780
QY 781 NGVNVISGPIFDYDGLHEDTKIKYVEGSSIPVPHYYSIITSCLDFTQPADKCDGP 840
Db 781 NGVNVISGPIFDYDGLHEDTKIKYVEGSSIPVPHYYSIITSCLDFTQPADKCDGP 840
QY 841 LSVSSFTLPHRPNDEESCSNDESKWVEELMKMHTARVRIEHLTSLDFFRKTSSRYPE 900
Db 841 LSVSSFTLPHRPNDEESCSNDESKWVEELMKMHTARVRIEHLTSLDFFRKTSSRYPE 900
QY 901 ILTKYLYHTYSEI 915
Db 901 ILTKYLYHTYSEI 915

RESULT 2

A55453
N: Contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1)
C: Species: Rattus norvegicus (Norway rat)
C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C: Accession: A55453; J00187
R: Narita, M.; Goji, J.; Nakamura, H.; Sano, K.
J. Biol. Chem. 269, 28235-28242, 1994
A: Title: Molecular cloning, expression, and localization of a brain-specific phosphodiesterase I (EC 3.1.4.1)
A: Reference number: A55453; MUID: 95050605
A: Accession: A55453
A: Molecule type: mRNA
A: Residues: 1-885 <NR>
A: Cross-references: GB:D28560; NID:g464196; PIDN:BAA05910.1; PID:g464197
R: Narita, M.; Goji, J.; Sano, K.; Nakamura, H.
submitted to JIPID, February 1994

A: Description: Cloning and expression of brain-specific nucleotide diphosphohydrolase
A: Reference number: J00187
A: Accession: J00187
A: Molecule type: mRNA
A: Residues: 1-86, 'Q', '88-81, 'T', '83-94, 'C', '96, 'A', '98-195, 'A', '197-514, 'E', '516-621, 'E', '62
A: Experimental source: strain Sprague-Dawley
C: Superfamily: nucleotide pyrophosphatase; somatostatin B homology
C: Keywords: coenzyme A; exonuclease; glycoprotein; phosphoprotein; phosphoric diester
E: 54-97/Domain: somatostatin B homology <SBH1>
E: 98-141/Domain: somatostatin B homology <SBH2>
E: 150, 396, 408, 522, 608, 829/Binding site: carbohydurate (Asn) (covalent) #status pred
F: 207/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 85.8%; Score 4306; DB 1; Length 885;

Best Local Similarity 83.6%; Pred. No. 1.7e-287;

Matches 792; Conservative 33; Mismatches 28; Indels 94; Gaps 6;

QY 1 MARRSSFOQCIIISLFTFAVGVISICLGTAAHRIKRAEGWEEGPTVLSDSPMTNIGSCK 60
Db 1 MARQCLGSGFQVLSLFTFAISVNICLGTASRIKRAE-WDEGPTVLSDSPMTNIGSCK 59
QY 61 GRCFELQEAAGPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDCRGEVRNEENACHC 120
Db 60 GRCFELQEAAGPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDCRGEVRNEENACHC 119
QY 121 SEDCLARGDCCNYQVVKGESHVDD-----DCEEIKAAECAPGAFVPPPLIIFSVG 173
Db 120 PEDCLSRGDCCTNYQVVKGESHVDDAARNOSSECLQV-----CP-----PPLIIFSVG 170
QY 174 FRASYMKGSKVMPNIEKLRSCGTHSPYMRVYTKFPNLYTLATGLYPESHGIVGNSM 233
Db 171 FRASYMKGSKVMPNIEKLRSCGTHSPYMRVYTKFPNLYTLATGLYPESHGIVGNSM 230
QY 234 YDVFDAFTHLGRKFNHRWGGQPLWITATKGVAGTFFWVVIPIHERRILTLRLW 293
Db 231 YDVFDAFTHLGRKFNHRWGGQPLWITATKGVAGTFFWVVIPIHERRILTLRLW 290
QY 294 TLPDHERPSVYAFYSEQDFSGHKYGFPGPPESSYSGPFPAPKRPKRVAPKRRQERVA 353
Db 291 SLPDNERPSVYAFYSEQDFSGHKYGFPGPPESSYSGPFPAPKRPKRVAPKRRQERVA 321
QY 354 PPKRRRKTHRMDDHAAETRODKMTNPLREIDKIVGQMLGKQLKLRRCVNVIPVGDH 413
Db 322 -----MTNPLREIDKIVGQMLGKQLKLRRCVNVIPVGDH 358
QY 414 MEDVTCDRTEFLSNLTNVDDITLVPGLTGRIRKFSNNAKYDPKAIITANLTCKPDQHF 473
Db 359 MEDVTCDRTEFLSNLTNVDDITLVPGLTGRIRKFSNNAKYDPKAIITANLTCKPDQHF 418
QY 474 KPYLQHLKRLHYANNRRIEDIHLVRRWHVARKPLDVYKPKSGKCFQGDHGFNDKV 533
Db 419 KPYLQHLKRLHYANNRRIEDIHLVRRWHVARKPLDVYKPKSGKCFQGDHGFNDKV 478
QY 534 NSMQTVFVGYGPTFKYTKVPPFENIELYNVWCDLGLKLPAPNNGTHGSLNHLRTNFR 593
Db 479 NSMQTVFVGYGPTFKYTKVPPFENIELYNVWCDLGLKLPAPNNGTHGSLNHLRTNFR 538
QY 594 PTMPEVTRPNYPGIMYLSQDFDLGCTCDDKVEPKNLDELKRLHTKGTSE----- 645
Db 539 PTMPEVTRPNYPGIMYLSQDFDLGCTCDDKVEPKNLDELKRLHTKGTSEATCKFRG 598
QY 646 -----ERHLLYGRPAVLRYRDIYTLHTDPSGYSEIFLMLLTSTYV 688
Db 599 SKHENKKNLNGSVPEKRRHLLYGRPAVLRYRDIYTLHTDPSGYSEIFLMLLTSTYV 658
QY 689 SKQAEVSSVPDHLTSCVRPDRVYSPFSQNCIAYKNDKQMSYGFLLPPLYLSSSPEAKYDA 748
Db 659 SKQAEVSSVPDHLTSCVRPDRVYSPFSQNCIAYKNDKQMSYGFLLPPLYLSSSPEAKYDA 718
QY 749 FLVITNNVMPYPAKRVWNYQFQVLVKKYASERNGVNVISGPIFDYDGLHEDTKIKY 808
Db 719 FLVITNNVMPYPAKRVWNYQFQVLVKKYASERNGVNVISGPIFDYDGLHEDTKIKY 778

[illegible]

Qy	513	VYKPSGCKFQGHDGNKVNSMQTVFGVGGPTFKTKVPPEENIELYNVMCDLGLK	572
Dd	472	--NKSSNC--EGGTHGVNFEKSMEAIFLAHGPSFKETKTVEPEENIEVNLLCDLHLHIQ	528
Qy	573	PAPNGTHGSUNHLLRTNTFRPTPEEVTRPNYPGIMVLQSDFDLCTCDDKVEPKNKLD	632
Dd	529	PAPNNGSHGSUNHLLKAPFYQSHAELSUSAGCGFTTLPKDSLNSC--IALQTSQEE	587
Qy	633	ELNRLLHTKG----STEERHILLYGRPAVLRYRTR--YDILYHTDFSGYSEIFLMLLWTSYT	687
Dd	588	QVNQRNLNSGGVESATEKTNLPFCRPRIQKNKDCHLLYHREYVSGFGAKMKMPMWSYTT	647
Qy	688	VSKOAEVSSPDHLTSCVRPDRVRSFESQNCLAYKNDKQMSYGFLPPPYLSSSPEAKYD	747
Dd	648	VPKPGDTSSLPTVPDCLRADRVDPSPESCQCSFLADQNTDHGFLYPPAIKGNSESQYD	707
Qy	748	AFLTNNVPMYPAPFKRWNYFORVLVKYASERNGVNVISGPIDYDYDGLHDTEDKIQ	807
Dd	708	ALITSNLVPMTEKKRMWDYFHKLVIKIAIERNGVNVVSGPIFDYNDGHFDAPDEITN	767
Qy	808	XVEGSSIPVPHYYITSCLDFTQPADCDCGPLSVSFSFILPHRPDNEESCENSESKW	867
Dd	768	XVACTDVPVPTHFYFWLTSCNKHHTPDSPCFGDLVDLPFVVPHRPTNVESPENKAEDLW	827
Qy	868	VEELMKMHTARVRDIHEHTSLDFFPRKSRSYPEILTKTYLHTHYESEI	915
Dd	828	VEERFKAHARVRDELTLGLDFYQEKTPQPVSEILQLKTLVLTPTETII	875

RESULT 4

A39216 plasma cell membrane glycoprotein PC-1 - human
N;Contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1)
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-May-2000
C;Accession: A39216; S21706; S23587; S51030
R;Buckley, M.F.; Loveland, K.A.; McKinstrey, W.J.; Garson, O.M.; Goding, J.W.
J. Biol. Chem. 265, 17506-17511, 1990
A;Title: Plasma cell membrane glycoprotein PC-1. cDNA cloning of the human molecule,
A;Reference number: A39216; MUID:91009202
A;Accession: A39216
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-925 <BUCC>
A;Cross-references: GB:J05654
R;Funakoshi, I.; Kato, H.; Horie, K.; Yano, T.; Hori, Y.; Kobayashi, H.; Inoue, T.; S
Arch. Biochem. Biophys. 295, 180-187, 1992
A;Title: Molecular cloning of cDNAs for human fibroblast nucleotide pyrophosphatase.
A;Reference number: S21706; MUID:92246539
A;Accession: S21706
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-925 <FUN1>
A;Accession: S23587
A;Molecule type: protein
A;Residues: 116-121;247-271,'X',273-275;279-280,'X',282-283;303-316;362-364;449-465;4
A;Note: it is uncertain whether Met-1 or Met-53 is the initiator
R;Bell, S.I.; Goding, J.W.
Eur. J. Biochem. 226, 433-443, 1994
A;Title: Biochemical characterization of human PC-1, an enzyme possessing alkaline ph
A;Reference number: S51030; MUID:95094801
A;Accession: S51030
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-80 <BEL>
C;Genetics:
A;Gene: GDB:PDNP1; M6S1; NPPS
A;Cross-references: GDB:132615; OMIM:173335
A;Map position: 6q22-6q23
C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C;Keywords: coenzyme A; glycoprotein; phosphoprotein; phosphoric diester hydrolase;
F:77-97/Domain: transmembrane #status predicted <TM>

RESULT 8

T03293
nucleotide pyrophosphatase homolog - rice
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
R:Accession: T03293
R:Hsing, Y.C.; Tsao, C.V.; Chow, T.; Hsieh, J.; Chen, Z.
submitted to the EMBL Data Library, April 1995
A:Description: Rice early embryogenesis gene.
A:Reference number: 214889
A:Accession: T03293
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-479 <HSI>
A:Cross-references: EMBL:U25430; NID:g818848; PID:g818849
A:Experimental source: strain Tainung 67
C:Genetics:
A:Note: OSE4

Query Match 12.2%; Score 611.5; DB 2; Length 479;
Best Local Similarity 31.4%; Pred. No. 2.5e-34;
Matches 150; Conservative 65; Mismatches 132; Indels 131; Gaps 14;
QY 152 IKAACPCAGFVR-----PPLIIFSVGDFRASYMKKSKYMPNIEKLRSCGTHSPY-MR 203
Db 71 LSAAPAPAAARAAQVLEKPVVILISSDGRFRGQHKAA--TPHTRHIGNGTSAATGLV 128
QY 204 PVYPTKTPNLYLTATGLYPESHGIVGNSMDPVPDATFHLGRKGFNRHWGGOLWIT 263
Db 129 PIFPTLFPNHYSTATGLYPESHGIIINYPDPISGDYFTWSSHEP---KMWLGEPLWYT 185
QY 264 ATKGVKAGGFFW-----SVVIPHERILLTLRLWTLDPDHERPSV 303
Db 186 AADGIGAAITFGSEVKKGSWCDPKYCHRYNGSVFEEERVDAILGVFDLPSEMPQF 245
QY 304 YAFYSEOPDFSGHYKPGFPPESSYSGPPTPAKRPKRKRVAPKRRQERPVPAPKRRKTIH 363
Db 246 LTLFEDPDHGHQGVDPD----- 265
QY 364 RMDHYAAETRODKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCR-- 421
Db 266 -----AITEAVRIDEIGRLIAGLEERGVEFVNVILVGRGMVG--TCDKKL 312
QY 422 -----TEFLSNLYTNVDDITLVPTGLGRIRSKSPNNAKYDPKATII 461
Db 313 VFDELAPWIKLEEDWVLSWTPLLA--IRPPDDMSL--PDVAKMNEGLSGSK-----V 362
QY 462 ANLTCKPQDQHFKPKLKOHLPKRLHYANNRRIEDIHLVERRWHVARKPLDVKYKPSGKC 521
Db 363 EN-----GEYLRMYLKEDLPSRLHYADSYRIPPIIGLPEEGYKVKEMKRS--KNECG-- 412
QY 522 FFOGDHGVKNVSMQTVFVGYGTFYKTKVPPENIELYNVMDLIGLKPAPNNGT 579
Db 413 ---CAHGYDNAFFSWRTIFIAHGRFEGGVVPSPEVNIYNIASILNLEPAPNGS 467

RESULT 9

T19494
hypothetical protein C27A7.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
R:Accession: T19494
R:Harris, B.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19132
A:Accession: T19494
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-829 <WIL>
A:Cross-references: EMBL:Z81041; PIDN:CA802784.1; GSPDB:GN00023; CESP:C27A7.1
A:Experimental source: clone C27A7
C:Genetics:

A:Gene: CESP:C27A7.1

A:Map position: 5
A:Introns: 12/3; 37/1; 100/3; 176/2; 272/3; 392/1; 427/1; 479/2; 566/2; 588/3; 677/1;
Query Match 12.2%; Score 610; DB 2; Length 829;
Best Local Similarity 23.9%; Pred. No. 6.5e-34;
Matches 192; Conservative 127; Mismatches 278; Indels 208; Gaps 31;
QY 139 KGESHVWDDDCCEIKAAECPCAGFVRPPLIIFSVGDFRASYMKKSKYMPNIEKLRSCGTH 198
Db 158 KARYEW--KGQNLGKCEL--SGYTKPPLVILSLDGFAREYVDR--NIVOTLNHIADCGVK 212
QY 199 SPYMRPVYPTKTPNLYLTATGLYPESHGIVGNSMDPVPDATFHLGRKGFNRHWGGQ 258
Db 213 ADKVPSYPSKTPPNHYSTVITGLWPESHGITNSVDFPTISPVLESMMKSTKY-EKFEFE 271
QY 259 PLW-ITATKQGVKAGTFFW-----SVVIPHERILLTLRLWTLDPDHE 299
Db 272 PIWSVTKRKTKGKCANCLFWVGCAYNNSGYADPAPAYNOELPFRNRIDTVVEWLKLPVE 331
QY 300 RPSVYAFYSEOPDFSGHYKPGFPPESSYSGPPTPAKRPKRKRVAPKRRQERPVPAPKRR 359
Db 332 RPLITAYLHEPDNACH----- 348
QY 360 RKIHRMDHYAAETRODKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTC 419
Db 349 ---QYVD-----EEDVDEKLAIEDENLDYLSRLSEKLECFINFAILSDHGMQLI-- 396
QY 420 DRTEFTSNLYTNVDDITLVPTGLGRIRSKFSNNAKVDPKAIANILCKKQDQHFKPYLKQ 479
Db 397 DKTYYPQDYL-DLKGLITAKGVVGRV---YINDTTISVNDVVDKFRCK--IDTVKNTNRS 450
QY 480 HLPKRLHYANNRRIEDIHLVERRWHVARKPLDVKYKPSGCFEGDGHGDNKVNSMQTV 539
Db 451 DVPTRKHYGRDPKVGVE--LLE-----GRAGVTYKSKADDYELSGDHGYDYFNPKMHTI 503
QY 540 FVGYGTFYKTKVPPENIELYNVMDLIGLKPA--PNNGTHGSLNHLRLTNTFRPTMPE 598
Db 504 FYARGSFQNTTISPYQNIQYMNLMWNLGIEGAVETNGTIGFFDNIL--TNPPRDNPT 562
QY 599 EVTRP-----NYPGIMYLSQDFDLCCTCDKVEPKNKLDELNKLRLHTKGTSEERHLLYGRP 654
Db 563 NVIGECPMIAFSPV-----LKCNGNVAETLNLQ-----SVKLNCAFSPT 603
QY 655 AV-LYTRFDILYHTDFESGYSEIFLMLLWTSYTSKQA-----EVSSVDPDH 700
Db 604 NIPLYSDNHCFOYCD-----NSVIVSRKGNDAARRAIEVLRSDEASNPNS 649
QY 701 LTSCVRPDRVRSFSONC-----LAYKNDKQMSYGFPPPYLSSSPKAYDA---F 749
Db 650 FTF-----LNKAYOSNCPSHIPTGSLTIQNSQ-----LSSMYDERIDVPPNF 692
QY 750 LVTNMVPMYPAFKRVNVYFORVLVKKYASERNGVNVISGPIFYDYDGLHDTEDKIQYV 809
Db 693 LLKVLDPQAQSMEXELNKKFGMY-----VISGATDINHDIADS----- 732
QY 810 EGGSIPTVPHYYSIITSC-----LDFTQPADKCDGPLSVSSSFIPLPHRPDNEESCNSSEDES 865
Db 733 NGSVI---THIYRIMLICNTSWLLMNPPLCTDSMDTUSFIFFPITEQSTDCMSSDD-- 787
QY 866 KWVEELMKWHTARVRDIEHLTSLDF 890
Db 788 -----ILLDYATATFDVERISGQF 807
RESULT 10
T09933
nucleotide pyrophosphatase homolog T16L4.210 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
R:Accession: T09933
R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.

A;Map position: 4

233 LVKIDQITGQLVQGLKQGIK⁻-ANLVIVSDHGMAATSSDRVVALNKNILDFSLIHVVIGG 290

QY 665 LYHTDFESGYSEIFLMLLWTSYTSVSKQAEVSSVPDHLTSCVRPDR-----VSPSFQSN 718
Db 518 --NNCFQS-YCE-----NSLIHKN-----RQDVKGVIESITFSFRN 553
QY 719 CLAYKNDQMSYGFLEPPY-----LSSSPEAKY---DAFLVTNMV 755
Db 554 QSVFEN-----SFSFYNTKYSIECPKIDTKDNFTAGSEAIKLANAQYKFPSPSEKSELI 609
QY 756 PMPYPAFK-----RWNYFQRLVVKKYASERNVNSGPIFDYDYGHLHTED 803
Db 610 SSLJSLKDTIKFVDIWNPLS--IKTDEYLKHYGKLFVLSGLAVDRNLGDADDEE 663

RESULT 15
A41179
Protein kinase PC-1 (EC 2.7.1.1) - bovine (fragments)
N:Alternate names: MAFP; major acidic fibroblast growth factor-stimulated phosphoprotein
C:Species: Bos primigenius taurus (cattle)
C:Date: 28-May-1992 #sequence_revision 22-Apr-1995 #text_change 30-Apr-1999
C:Accession: A41179; A49308
R:Oda, Y.; Kuo, M.D.; Huang, S.S.; Huang, J.S.
J. Biol. Chem. 266, 16791-16795, 1991
A:Title: The plasma cell membrane glycoprotein, PC-1, is a threonine-specific protein kinase
A:Reference number: A41179; MUID:91358477
A:Accession: A41179
A:Molecule type: protein
A:Residues: 1-26;36-56;59-67;68-133;134-144;145-267;268-300 <ODA>
A:Experimental source: liver
R:Oda, Y.; Kuo, M.D.; Huang, S.S.; Huang, J.S.
J. Biol. Chem. 268, 27318-27326, 1993
A:Title: The major acidic fibroblast growth factor (aFGF)-stimulated phosphoprotein from
estrase activities.
A:Reference number: A49308; MUID:94086550
A:Accession: A49308
A:Molecule type: protein
A:Residues: 27-35,'X',37-58 <OD2>
A:Experimental source: liver
A:Note: sequence extracted from NCBI backbone (NCBIP:141583)
C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C:Keywords: glycoprotein; phosphoprotein; phosphotransferase
F:1-25/Domain: somatomedin B homology (fragment) <SBH>
F:36/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 9.1%; Score 456; DB 2; Length 300;
Best Local Similarity 18.7%; Pred. No. 6.3e-24;
Matches 150; Conservative 45; Mismatches 86; Indels 522; Gaps 14;

QY 107 RCGEVRNEENACHCEDCLARGDCCTNYQVCKGSHWVDDCEIEKAAECFAGFVRPPL 166
Db 2 RCFE-RTEFGN-CRCDAACVELGNCLD----- 26
QY 167 IIFSVDGFRASYMKKSGKMPNIEKLRSCGTHSPYMPVYPTKTPNLYTLATGLYPESH 226
Db 27 -----NRPVYPTKTPNHYSIIVTGLYPESH 52
QY 227 GIVGNSMYDPVDFATFHLRGRKFNHRWVGQPLWITATKQGVKAGTFWF----- 276
Db 53 GIIDNK-----GEPIWLTA-----KSGTFWPGSDVKINGI 83
QY 277 -----SVVIPHERILLTLRWITLDPHERPSVAFYSEQPDFSGHKYGFPGPEESSYSGP 331
Db 84 FPDYXVSVPFEEIRLAILKWLQP----- 108
QY 332 FPAKRPKPKVAPKRQRPVAPPKRRRK IHRMDHYAAETQDKMTNPLREIDKIVGQL 391
Db 109 ----- 108
QY 392 MDGLKLRRCVNVIFYDGHGMDVTCDRTEFLSNLYTNVDDITLVPCTGLGRIRSKFSN 451
Db 109 ----KELNLHCLNLLISDHGMEGSCKYYSF-----DYEG 141

QY 452 NAKYDPKAIITANLTCKKPDQHFEPYLKQHLPKRLHYANNRRIEDIHLVERHWARKPL 511
Db 142 IAKSD-----RIERLTFYLDQWQWALNPS 166
QY 512 DVYKKPSGCKFFOGDGHGFDNKNVSMQTVFVGYGTFYKTKVPPFENIELYNVWCDLLGL 571
Db 167 E--RKYG-----GGFHGSDNLFNMQALFXXXXXXHSHTEVDSFENIEVYNLMCDLLNL 220
QY 572 KPAPNNGTHGSLNHLNTFRPTMPEVTRPNYPGIMYLQSDFDLGCTCDCKVEPKNKL 631
Db 221 TPAPNNGTH----- 229
QY 632 DELNKLHTRKSGSTEERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTSVKQ 691
Db 230 ----- 229
QY 692 AEVSSVPDHLTSCVRPDRVSPFSQNCLAYKNQKMSYGFLFPPYSSSPEAKY-DAFL 750
Db 230 -----LSYGLSPQLHKGSSQVYSEALL 253
QY 751 VTNNVPMYPAFKRVWNYFQRLVVKKYASERNVNSGPIFDYDYGHLHTEDKIKQYVE 810
Db 254 TTNIVPMYQSFQVI----- 267
QY 811 GSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCNSDESKWVEE 870
Db 268 -----HESLWVEE 275
QY 871 LMKMHTARVRDIEHLTSLDFFRK 893
Db 276 LLKLHTARITDVEHITGLSFYQQ 298

Search completed: July 19, 2001, 14:45:54
Job time: 152 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:44:18 ; Search time 16.91 Seconds
(without alignments)
1853.564 Million cell updates/sec

Title: US-09-483-831-69
Perfect score: 5019
Sequence: 1 MARRSFQSQIISLTFV.....RSYPILTLKYLHTESEI 915

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1955.5	39.0	873	1 PCL_HUMAN	P22413 homo sapien
2	1899.5	37.8	871	1 PCL_MOUSE	P06802 mus musculus
3	410	8.2	743	1 YCB6_YEAST	P25353 saccharomyc
4	335.5	6.7	493	1 YEB6_YEAST	P39997 saccharomyc
5	238	4.7	61	1 PPDI_BOVIN	P15396 bos taurus
6	146.5	2.9	329	1 NUC1_YEAST	P08466 saccharomyc
7	123	2.5	4655	1 LRP2_HUMAN	P98164 homo sapien
8	122	2.4	1323	1 YD23_CAEEL	P24348 caenorhabdi
9	121	2.4	1888	1 YD22_SCHPO	O14207 schizosacch
10	119.5	2.4	252	1 NUC1_CUNEE	P81203 cunningham
11	119.5	2.4	475	1 VTNC_RABIT	P22458 oryctolagus
12	117	2.3	335	1 NUC1_SCHPO	Q10480 schizosacch
13	116.5	2.3	989	1 YD30_YEAST	P32898 saccharomyc
14	112	2.2	1394	1 TGFH_HUMAN	P22064 homo sapien
15	111.5	2.2	299	1 NUCG_BOVIN	P38447 bos taurus
16	111	2.2	1396	1 ITA2_DROME	P12080 drosophila
17	111	2.2	2871	1 FBNI_HUMAN	P35555 homo sapien
18	110.5	2.2	294	1 NUCG_MOUSE	O08600 mus musculus
19	110.5	2.2	478	1 VTNC_MOUSE	P29788 mus musculus
20	110.5	2.2	2871	1 FBNI_BOVIN	P98133 bos taurus
21	110	2.2	753	1 YJ05_CAEEL	O01975 caenorhabdi
22	109.5	2.2	1472	1 ATC9_YEAST	Q12697 saccharomyc
23	108.5	2.2	320	1 NUC1_SYNRA	P81204 syncephalac
24	108	2.2	1065	1 YD22_SCHPO	O13710 schizosacch
25	106	2.1	1106	1 STC_DROME	P40798 drosophila
26	106	2.1	1178	1 YNI7_YEAST	P48231 saccharomyc
27	106	2.1	2204	1 RRPL_NDVB	P11205 newcastl d
28	106	2.1	2871	1 FBNI_MOUSE	Q61554 mus musculus
29	106	2.1	3099	1 POLG_PENVM	O56075 p genome po
30	105.5	2.1	1612	1 MTDM_PARLI	Q27746 paracentrot
31	105.5	2.1	1808	1 TENA_CHICK	P10039 gallus gall
32	104.5	2.1	2201	1 TENA_HUMAN	P24821 homo sapien
33	104.5	2.1	4289	1 TENX_HUMAN	P22105 homo sapien

RESULT 1

ID	PCL_HUMAN	STANDARD;	PRT;	873 AA.
AC	P22413; Q9Y6K3; Q9UP61;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1 [INCLUDES: ALKALINE			
DE	PHOSPHODIESTERASE I (EC 3.1.4.1); NUCLEOTIDE PYROPHOSPHATASE			
DE	(EC 3.6.1.9) (NPPASE)].			
GN	PDNPI OR PCL OR NPPS.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91009202; PubMed=2211644;			
RA	Buckley M.F., Loveland K.A., McKinstry W.J., Garson O.M., Goding J.W.;			
RT	"Plasma cell membrane glycoprotein PC-1, cDNA cloning of the human			
RT	molecule, amino acid sequence, and chromosomal location.";			
RL	J. Biol. Chem. 265:17506-17511(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92246539; PubMed=1315502;			
RA	Funakoshi I., Kato H., Horie K., Yano T., Hori Y., Kobayashi H.,			
RA	Inoue T., Suzuki H., Fukui S., Tsukahara M., Kajii T.,			
RA	Yamashina I.;			
RT	"Molecular cloning of cDNAs for human fibroblast nucleotide			
RT	pyrophosphatase.";			
RL	Arch. Biochem. Biophys. 295:180-187(1992).			
RN	[3]			
RP	SEQUENCE OF 93-133 FROM N.A., AND VARIANT GLN-121.			
RX	MEDLINE=99408501; PubMed=10480624;			
RA	Pizzuti A., Frittitta L., Argiolas A., Baratta R., Goldfine I.D.,			
RA	Bozzali M., Ercolino T., Scarlato G., Iacoviello L., Vigneri R.,			
RA	Tassi V., Trischitta V.;			
RT	"A polymorphism (K121Q) of the human glycoprotein PC-1 gene coding			
RT	region is strongly associated with insulin resistance.";			
RL	Diabetes 48:1881-1884(1999).			
CC	-!- FUNCTION: MAY HAVE A ROLE IN THE REGULATION OF N-GLYCOSYLATION.			
CC	-!- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES			
CC	SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED			
CC	OLIGO-NUCLEOTIDES.			
CC	-!- CATALYTIC ACTIVITY: A DINUCLEOTIDE + H(2)O = 2 MONONUCLEOTIDE.			
CC	-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.			
CC	-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.			
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN PLASMA CELLS AND ALSO IN A NUMBER			
CC	OF NON-LYMPHOID TISSUES, INCLUDING THE DISTAL CONVOLUTED TUBULE			
CC	OF THE KIDNEY, CHONDROCYTES, AND EPIDIDYMIS.			
CC	-!- SIMILARITY: CONTAINS 2 SOMATOMEDIN-B TYPE DOMAINS.			
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CC	use by non-profit institutions as long as its content is in no way			

P38934 saccharomyc
P18791 streptococc
P13677 drosophila
P33538 neurospora
Q14249 homo sapien
P52519 human herpe
Q03376 chironomus
P21128 homo sapien
P06971 escherichia
P04412 drosophila
Q08890 mus musculu
P14738 staphylococ

ALIGNMENTS

RA	Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
RL	-I- SIMILARITY: TO YEAST YCR26C.
CC	-----
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CC	-----
DR	EMBL; U18530; AAB64493.1; --.
DR	SGD; S0000742; YEL016C.
DR	InterPro; IPR002591; --.
DR	pfam; PF01663; Phosphodiesterase 1.
KW	Hypothetical protein.
SQ	SEQUENCE 493 AA; 57354 MW; 10E67A05C6DEDFO9 CRC64;

	Query Match 6.7%; Score 335.5; DB 1; Length 493; Best Local Similarity 24.8%; Pred. No. 7.6e-17; Matches 116; Conservative 71; Mismatches 153; Indels 127; Gaps 21;
QY	167 IIFSVDGFRASYM-KKGSKNVPNTEKLRSCG----THSPYMRRPVYPKTFFNLTYLATGL 221 : : : : : : : : : : : : : Db 79 ILISIDGFHPLDAKYTFPFLYNHLNRSLPSYDMITAPYMPISFPTQTTPFNHWSMVTKG 138
QY	222 YPESHGIVGNMSVDPVDATPHLRGREKFNRHWG--GQLPW--ITATKQG-VRAGTFFFW 276 : : : : : : : : : : : : : : : Db 139 YPIEHGIYSNIWFNDFTSSEFR---PNMLDARIWSNTADPIWLQLLTQSQQGYKVATHMW 195
QY	277 ---SVV-----IPHER-----RIILTIRLWTLPD-HERPSVYAFYSEQ 310 : : : : : : : : : : : Db 196 PGSEVVVEDHGSDVRERPFPFGFKNQWEKLQDLAQIFRYIDMPQLKDREPLVISYIPN 255
QY	311 PDFSGKHGVPGPESSYSGSPTPAKRPKRVAPRKQRQERVAPPKKRRRIHRMDHYAA 370 : : : : : : : : : : Db 256 VDSYGHSFG-----Y 265
QY	371 ETRODKTNPIREDIKVGQLMDGLKQLBRCNVNFVGDHGMEDVTCRDTEF----- 424 : : : : : : : : : : : : : : Db 266 DLDRKRLQKLIGEVDGFFLDIEGLQRKNLLKISNMVISDHGSMNNVANDEGHVVMWER 325
QY	425 -----LSNYLTNVDDITLVPGTLGRISRKSNAKYDPKAIANLTCCKPDQ---HFKP 475 : : Db 326 VFPADAMSAPISHLYN---EGPMWVCWKNPDKOWICLDLEAQLEYAGDEISRKEFHV 381
QY	476 YLKQHLP---RELHYANNR-----RIEDIHLVERRWHVARKPLDVYKKPGSKCFQGDH 527 : : : : : : : : : : : : : : Db 382 ILKEDFDPSWKYFYQDNKRKHRYDDRVRGDIWLADEYYAIVKMGDV---PIG---IMGTH 435
QY	528 GFD-NKVNMQTVFGYGTPTYKYTKVPPFENIELYNMCD---LLG 570 : : : : : : : : : : : : : : : : : : : Db 436 GYNFNCSDMAISFITGMGPFMNEEV-YPFENIEVINLIKASALLG 481

RESULT	5
PPDJ_BOVIN	
ID	PPDJ_BOVIN STANDARD; PRG; 61 AA.
AC	P15396;
DT	01-APR-1990 (Rel. 14, Created)
DT	01-APR-1990 (Rel. 14, Last sequence update)
DT	01-FEB-1994 (Rel. 28, Last annotation update)
DE	PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-NUCLEOTIDE DE PHOSPHODIESTERASE) (FRAGMENT).
OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX	Bovidae; Bos.
RN	[1]

RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=85234541; PubMed=2989287;
 RA Culp J.S., Blytt H.J., Hermodson M., Butler L.G.;
 RT "Amino acid sequence of the active site peptide of bovine intestinal
 RT 5'-nucleotide phosphodiesterase and identification of the active
 RT site residue as threonine.";
 RL J. Biol. Chem. 260:8320-8324(1985).
 CC -1- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
 CC SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
 CC OLIGO-NUCLEOTIDES.
 DR PIR: A25274; A25274.
 KW Hydrolase.
 FT NON_TER 1 1
 FT ACT_SITE 39 39 FORMS A PHOSPHOTHREONINE INTERMEDIATE.
 SQ SEQUENCE 61 AA; 6999 MW; 580C8B4807A61C84 CRC64;
 Query Match 4.7%; Score 238; DB 1; Length 61;
 Best Local Similarity 66.7%; Pred. No. 5.4e-11;
 Matches 40; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 QY 172 DGFRAHYMKGKGVNPKLRSCGTHSPYMPVYTKFPNLYTLATGLYPESHGIVGN 231
 Db 1 DGFRAEYQTWSTLVNPKLRGTHSPYMPVYTKFPNLYTLATGLYPESHGIVGN 60
 RESULT 6
 NUC1_YEAST
 ID NUC1_YEAST STANDARD; PRT; 329 AA.
 AC P08466;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE MITOCHONDRIAL NUCLEASE (EC 3.1.30.-).
 GN NUC1 OR YJL208C OR J0310 OR HRE329.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2935-106;
 RX MEDLINE=88233924; PubMed=2836792;
 RA Vincent R.D., Hofmann T.J., Zassenhaus H.P.;
 RT "Sequence and expression of NUC1, the gene encoding the mitochondrial
 RT nuclease in Saccharomyces cerevisiae.";
 RL Nucleic Acids Res. 16:3297-3312(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX MEDLINE=95274326; PubMed=7754713;
 RA Purnelle B., Coster F., Goffeau A.;
 RT "The sequence of a 36 kb segment on the left arm of yeast chromosome
 RT X identifies 24 open reading frames including NUC1, Prp21 (Spp91),
 RT CDG6, CRY2, the gene for S24, a homologue to the aconitase gene ACO1
 RT and two homologues to chromosome III genes.";
 RL yeast 10:1235-1249(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX MEDLINE=95242842; PubMed=7725802;
 RA Vandenbol M., Durand P., Bolle P.-A., Dion C., Portetelle D.,
 RA Hilger F.;
 RT "Sequence analysis of a 40.2 kb DNA fragment located near the left
 RT telomere of yeast chromosome X.";
 RL yeast 10:1657-1662(1994).
 RN [4]
 RP SEQUENCE OF 204-329 FROM N.A.
 RX MEDLINE=90014786; PubMed=2552292;
 RA Liu Y., Dieckmann C.L.;
 RT "Overproduction of yeast virulike particles by strains deficient in
 RT a mitochondrial nuclease.";

RL Mol. Cell. Biol. 9:3323-3331(1989).
 CC -1- FUNCTION: THIS ENZYME HAS BOTH RNASE AND DNASE ACTIVITY.
 CC -1- COFACTOR: REQUIRES MANGANESE OR MAGNESIUM.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE DNA/RNA NON-SPECIFIC ENDONUCLEASES
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL: X05670; CAA29870.1; -;
 DR EMBL: X77688; CAA54748.1; -;
 DR EMBL: Z34098; CAA84003.1; -;
 DR EMBL: Z49483; CAA89505.1; -;
 DR EMBL: M28067; AAA34457.1; -;
 DR PIR: S05888; NCBYNI.
 DR PIR: S46621; S46621.
 DR HSP: P13717; ISMN.
 DR SGD: S0003744; NUC1.
 DR InterPro: IPR001604; -;
 DR Pfam: PF01223; Endonuclease; 1.
 DR PROSITE: PS01070; NUCLEASE_NON_SPEC; 1.
 KW Hydrolase; Nuclease; Endonuclease; Magnesium; Mitochondrion;
 KW Inner membrane.
 FT ACT_SITE 138 138 BY SIMILARITY.
 SQ SEQUENCE 329 AA; 37209 MW; CAEC9678CB00943C CRC64;
 Query Match 2.9%; Score 146.5; DB 1; Length 329;
 Best Local Similarity 22.8%; Pred. No. 0.002;
 Matches 79; Conservative 48; Mismatches 159; Indels 61; Gaps 16;
 QY 565 MCDLLGLKAPNNGTHGSLNHLRTNFRTPMPEVTRPNYPGIMYLSQDFDLGCTCDK 624
 Db 1 MCSRIISGLVGLGAGTGLTYLL-LNKHSPT---OIETYP----- 38
 QY 625 VEPKNKLDLNLKRLTKGSTEERHLLYGRPAVLRYTRDILYHTDFESGYSEIFLMLWT 684
 Db 39 --PTQKNS-NIQSHSFNVDPGFGFKYGFPGPI---HDLQNRREFTSCYRQNTQNPVW 91
 QY 685 SYTVSKQAEVSSVPDHLTSCVPRDVRVSPFSQNLAYKNDKQMSYGLFPY-LSSSPE 743
 Db 92 LEHITPESLAARNADRNKNSFFKEDVPEKFRGLRDYFR-SGYDRGHQAPADAQKFSQ 150
 QY 744 AKYDAFLVTNMPMY-PAFKR-VW---NYFORVLVKKYASERNGVNVISGPIFDYDGL 798
 Db 151 AMDTFTYLSNCPQVGEFNRDYWAHLEYFCRLTKYKS---VRIVTGPLYLPKKDPI 206
 QY 799 HDTEDKIQVVEGS--SIPVTHYYSIITSLDFTQPADKCDGLPSVSSFLPHRP-DNE 855
 Db 207 -DNKFRVNYEIVGPPSIAVPTHEFKLIVAEAPTANPARE---DIAVAAFVLPNPSNE 262
 QY 856 ESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSSYPEIL 902
 Db 263 TKLTDFE-----VPIDALERSTGLELLQKVPSPKKAL 295
 RESULT 7
 LRP2_HUMAN
 ID LRP2_HUMAN STANDARD; PRT; 4655 AA.
 AC P98164; O00711; Q16215;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 PRECURSOR (MEGALIN)
 DE (GLYCOPROTEIN 330).
 GN LRP2.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RA MEDLINE=96305376; PubMed=8706697;
RA Hjaelm G., Murray E., Crumley G., Harazim W., Lundgren S., Onyango I.,
RA Ek B., Larsson M., Juhlin C., Hellman P., Davis H., Akerstrom G.,
RA Rask L., Morse B.;
RT "Cloning and sequencing of human gp330, a Ca(2+)-binding receptor
RT with potential intracellular signaling properties.";
RL Eur. J. Biochem. 239:132-137(1996).
RN [2]
RP SEQUENCE OF 2705-4453 FROM N.A.
RC TISSUE=Kidney;
RA Knaak C., Argraves W.S.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 3833-4453 FROM N.A.
RX TISSUE=Kidney;
RA MEDLINE=95048397; PubMed=7959795;
RA Korenberg J.R., Argraves K.M., Chen X.N., Tran H.,
RA Strickland D.K., Argraves W.S.;
RT "Chromosomal localization of human genes for the LDL receptor family
RT member glycoprotein 330 (LRP2) and its associated protein RAP
RT (LRPAP1).";
FT Genomics 22:88-93(1994).
RN [4]
RP SEQUENCE OF 4139-4406 FROM N.A.
RX MEDLINE=94244704; PubMed=8187828;
RA Lundgren S., Hjaelm G., Hellman P., Ek B., Juhlin C., Rastad J.,
RA Klarekog L., Akerstrom G., Rask L.;
RT "A protein involved in calcium sensing of the human parathyroid and
RT placental cytotrophoblast cells belongs to the LDL-receptor protein
RT superfamily.";
RL Exp. Cell Res. 212:344-350(1994).
RN [5]
RP FUNCTION
RX MEDLINE=95286588; PubMed=7768901;
RA Kounas M.Z., Loukova E.B., Stefansson S., Harmony J.A.K.,
RA Brewer B.H., Strickland D.K., Argraves W.S.;
RT "Identification of glycoprotein 330 as an endocytic receptor for
RT apolipoprotein J/clusterin.";
RL J. Biol. Chem. 270:13070-13075(1995).
CC -!- FUNCTION: BINDS SPECIFICALLY CLUSTERIN WITH HIGH AFFINITY, BUT
CC ALSO LIGANDS IN COMMON WITH OTHER FAMILY MEMBERS: PLASMINOGEN,
CC EXTRACELLULAR MATRIX COMPONENTS, PLASMINOGEN ACTIVATOR-PLASMINOGEN
CC ACTIVATOR INHIBITOR TYPE I COMPLEX, APOLIPOPROTEIN E-ENRICHED
CC BETA-VLDL, LIPOPROTEIN LIPASE, LACTOFERRIN AND CALCIUM.
CC -!- FUNCTION: RECEPTOR-MEDIATED UPTAKE OF POLYBASIC DRUGS SUCH AS
CC APROTININ, AMINOGLYCOSIDES AND POLYMYXIN B (BY SIMILARITY).
CC -!- FUNCTION: MAY PARTICIPATE IN REGULATION OF PARATHYROID-HORMONE AND
CC PARA-THYROID-HORMONE-RELATED PROTEIN RELEASE.
CC -!- SUBUNIT: FORMS A MULTIMERIC COMPLEX TOGETHER WITH A RECEPTOR-
CC ASSOCIATED PROTEIN (RAP).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: ABSORPTIVE EPITHELIA, INCLUDING RENAL
CC PROXIMAL TUBULES.
CC -!- SIMILARITY: CONTAINS 36 LDL-RECEPTOR CLASS A DOMAINS.
CC -!- SIMILARITY: CONTAINS 37 LDL-RECEPTOR CLASS B DOMAINS.
CC -!- SIMILARITY: CONTAINS 17 EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 4 SH3-BINDING DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 SH2-BINDING DOMAIN.
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DR EMBL; U03837; AAB41649.1; -;
DR EMBL; U04441; AAB02882.1; -;
DR EMBL; S73145; AAB30825.1; -;
DR HSSP; P01130; IAJJ.
DR MIM; 600073; -;
DR InterPro; IPR000033; -;
DR InterPro; IPR000152; -;
DR InterPro; IPR000561; -;
DR InterPro; IPR001891; -;
DR InterPro; IPR002172; -;
DR Pfam; PF00008; EGF_1; 1.
DR Pfam; PF00057; ldl_recept_a; 36.
DR Pfam; PF00058; ldl_recept_b; 37.
DR PRINTS; PR00261; LDLRECEPTOR.
DR PROSITE; PS00010; ASX-HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 9.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS01209; LDLRA_1; 31.
DR PROSITE; PS50068; LDLRA_2; 36.
KW Glycoprotein; Repeat; Endocytosis; Coated pits; Transmembrane;
KW Receptor; EGF-like domain; Signal; Polymorphism.
FT SIGNAL 1 25
FT CHAIN 26 4655
FT DOMAIN 26 4423
FT TRANSMEM 4424 4446
FT DOMAIN 4447 4655
FT DOMAIN 26 64
FT DOMAIN 65 105
FT DOMAIN 106 144
FT DOMAIN 145 181
FT DOMAIN 182 219
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RT induction encodes a tyrosine kinase of the EGF receptor subfamily.;"

RL Nature 348:693-699(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=96177760; PubMed=8604137;
RA Sakai T., Koga M., Onshima Y.;

RT "Genomic structure and 5' regulatory regions of the let-23 gene in

RL the nematode *C. elegans*.";

RT J. Mol. Biol. 256:548-555(1996).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RA Thomas K.;

RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.

RN [4]

RP MUTANTS.

RX MEDLINE=94147981; PubMed=8313880;

RA Aroian R.V., Les G.M., Sternberg P.W.;

RT "Mutations in the *Caenorhabditis elegans* let-23 EGFR-like gene define

RL elements important for cell-type specificity and function.";

RT EMBO J. 13:360-366(1994).

CC -!- FUNCTION: TYROSINE KINASE RECEPTOR REQUIRED FOR THE INDUCTION OF
C.ELEGANS VULVA. POSSIBLE RECEPTOR FOR THE INDUCTIVE SIGNAL
REQUIRED FOR VULVAL DEVELOPMENT. ACTIVATED BY LIN-3 AND ACTS BY
WAY OF LET-60 RAS. THE LIN-3/LET-23 PAIR IS A SIMPLIFIED VERSION
OF THE MAMMALIAN NEURGUIN-ERBB NETWORK.

CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +

CC PROTEIN TYROSINE PHOSPHATE.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
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or send an email to license@isb-sib.ch).

CC -----

DR EMBL; X57767; CAA40919.1; ALT_SEQ.

DR EMBL; D63426; BAA09729.1; ALT_INIT.

DR EMBL; Z70038; CAA93882.1; -.

DR PIR; S13422; S13422.

DR HSP; P11362; IFGI.

DR WormPep; ZK1067.1; CE03840.

DR InterPro; IPR000494; -.

DR InterPro; IPR000719; -.

FT	CARBOHYD	746	746	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	776	776	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARIANT	368	368	C -> Y (IN SY10).
FT	VARIANT	469	469	G -> R (IN MN216).
FT	VARIANT	700	700	C -> W (IN MN23).
FT	VARIANT	753	753	C -> Y (IN SY11).
FT	VARIANT	1065	1065	T -> I (IN SY16).
FT	VARIANT	1074	1074	G -> E (IN SY7).
SQ	SEQUENCE	1323	AA; 150510	MW; 6B0307EE5EFA99 CRC64;

Query Match 2.4%; Score 122; DB 1; Length 1323;

Best Local Similarity 18.4%; Pred. No. 0.73;

Matches 149; Conservative 106; Mismatches 290; Indels 264; Gaps 43;

QY	48	SDSPWNTINISGCK-----GRCFELQEAGPPDCRCDNLC-----KSYTSCC	87
Db	225	NKCKWGSNDQCORVYRVCPSQCFSNSTSSVEC-CDSACLGCTGCHGPKNCIACS	283
QY	88	HDDELCLKTARGWECKDRCGEV-----RNEENACHSEDC-----LARGDCCTWYQVY	137
Db	284	KVELDGIETCTPSRKIFNHNKTRLVFNPDGRYONGNHCVCPCPELLIENDVCVRH---	340
QY	138	CKGESHW--VDD--DCEEEKAAECPCAGFVRPPLIIFSDGFRASYMKGSKYMPNIEKLR	193
Db	341	CSDGHHYDATKDVRECEKCRSSCPK-----ICTVDGHLT-----NETLKNLEGE	386
QY	194	SGTSPYMRPVYPTKTFPNLYTLAT--GLYPESHGIVGNSMYPVPFDATEFH--LRGREKN	251
Db	387	QIDGH-----LIIEHAFTYQLKVLKIVSEYITVQQNFYDLKFLKNLQIIEGRKLHN	442
QY	252	HRWWSG-----QPLWITATKGVKAGTFWFSVVPHERRILITILRLTLPDHERPSVY	304
Db	443	VRWALAIYQCDDLEELSLNSKL-IKTG-----AVLIMKNHRLC-----	480
QY	305	AFYSEOPDFSGHKYGPFGPESSYSGSFTPAKPKKVPKRPQERPVAPPKRRKIHR	364
Db	481	--YVSKIDWS-----IITSKGDKNKPSLAIAEN-----	508
QY	365	MDHYAAETQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEF	424
Db	509	-DSKICETEQ-----RVCDK-----NCNKGWGWKEPEDCLECKT	542
QY	425	LSNYLTNVDDITILVPGTLGRIRSKFSNNA-KYDPKAIAN-----LTCKKPDQHFKPY	476
Db	543	WKSVGTCVEKC---DTKGFLRNQTSMKCERCSPCETCNGELGELDCLTCRH-----	590
QY	477	LKQHLPKRLHYAN-NRRIEDIHLLVERRHVARKPL--DVYKKPSGKCFQGDHGFDNKV	533


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FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 870 870 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 923 923 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1039 1039 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1394 AA; 152791 MW; DFFCA81A40B2C7D1 CRC64;

Query Match
Best Local Similarity 2.2%; Score 112; DB 1; Length 1394;
Matches 49; Conservative 17; Mismatches 48; Indels 92; Gaps 15;

Qy 44 PTVLSDPWNTSGS-----C-----KRCFELQAGPPD-CR---CDNLCKSYTSCC 87
Db 678 PSTCDEQCVNPGSVQCPCTGFRGNGQCLDVDECLEPNVANGDCSNLGSYMSC 737
Qy 88 H-----DFDEL-----CLKYARGWECT-----KDR----- 108
Db 738 HKGYTRTPDHKHCRIDECQGNLCVNGQCKNTGSEFRCTCGQGYQLSAKDQCEDIDEC 797
Qy 109 -----GEVNEENA-----C-----HCSE--DCL-----ARGDCT--NY 134
Db 798 QHRHLCAHGQCRNTEGSGFCVQCDQYRASGLGDHCDINECLEDKSVQCRGDCINTAGSY 857
Qy 135 QVCKGESHVWDDD--CEEIKAAECP 158
Db 858 DCTCP-DGFLDDNKTCQDINECEHP 882

RESULT 15
NUCG_BOVIN STANDARD; PRT; 299 AA.
AC P38447;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENDONUCLEASE G PRECURSOR (EC 3.1.30.-) (ENDO G).
GN ENDOG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93342514; PubMed=7688144;
RA Cote J., Ruiz-Carrillo A.;
RT "Primers for mitochondrial DNA replication generated by endonuclease
RT G.";
RL Science 261:765-765(1993).
RN [2]
RP SEQUENCE OF 49-75.
RC TISSUE=Liver, and Thymus;
RX MEDLINE=88198128; PubMed=3360771;
RA Moos M. Jr., Nguyen N.Y., Liu T.-Y.;
RT "Reproducible high yield sequencing of proteins electrophoretically
RT separated and transferred to an inert support.";
RL J. Biol. Chem. 263:6005-6009(1988).
RN [3]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC TISSUE=Heart;
RX MEDLINE=95175374; PubMed=7870594;
RA Gerschenson M., Houniel K.L., Low R.L.;
RT "Endonuclease G from mammalian nuclei is identical to the major
RT endonuclease of mitochondria.";
RL Nucleic Acids Res. 23:88-97(1995).
CC -1- FUNCTION: CLEAVES DNA AT DOUBLE-STRANDED (DG)N. (DC)N AND AT
CC SINGLE-STRANDED (DC)N TRACTS. IN ADDITION TO DEOXYRIBONUCLEASE
CC ACTIVITIES, ALSO HAS RIBONUCLEASE (RNASE) AND RNASE H ACTIVITIES.
CC CAPABLE OF GENERATING THE RNA PRIMERS REQUIRED BY DNA POLYMERASE
CC GAMMA TO INITIATE REPLICATION OF MITOCHONDRIAL DNA.
CC -1- COPACITOR: REQUIRES MANGANESE OR MAGNESIUM.
```

```
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -1- SIMILARITY: BELONGS TO THE DNA/RNA NON-SPECIFIC ENDONUCLEASES
CC FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X72802; CAA51320.1; -.
DR InterPro: IPR001604; -.
DR Pfam; PF01223; Endonuclease; 1.
DR PROSITE; PS01070; NUCLEASE_NON_SPEC; 1.
KW Hydrolase; Nuclease; Endonuclease; Mitochondrion; Transit peptide;
FT MAGNESIUM.
FT TRANSIT 1 48 MITOCHONDRION.
FT CHAIN 49 299 ENDONUCLEASE G.
FT ACT_SITE 143 143 BY SIMILARITY.
FT CONFLICT 172 172 H -> S (IN REF. 3; PROBABLE ERROR).
FT CONFLICT 264 264 H -> S (IN REF. 3; PROBABLE ERROR).
SQ SEQUENCE 299 AA; 32261 MW; B28FAFF56F04CFC7 CRC64;

Query Match
Best Local Similarity 2.2%; Score 111.5; DB 1; Length 299;
Matches 32; Conservative 24; Mismatches 41; Indels 27; Gaps 6;

Qy 741 SPEAKYDAFLVTNMVMPYPAF-KRWVN--YFQRLVKKYASERGVNVISGPIFDYD 796
Db 153 SQKAMDDTFYLSNVAPQVPHLNQANNNLEKYSRLTRY---QNVVCTGPLF----- 203
Qy 797 GLHDTEDKIQYVE-----GSSIPVPTHYYSITISCLDFTQPADKCDGSLVSSFILPHR 851
Db 204 -LPRTADGKSYKYQYVIGKNHVAVPTFFKVL-----LEAAGGQIELRSYVWNA 254
Qy 852 PDNE 855
Db 255 PVDE 258

Search completed: July 19, 2001, 14:47:09
Job time: 171 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:43:57 ; Search time 42.51 Seconds
(without alignments)
2847.779 Million cell updates/sec

Title: US-09-483-831-69
Perfect score: 5019
Sequence: 1 MARRSFQSQIISLFTFAV.....RSYPEILTKYLHTYESEI 915

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL16:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_unclassified:*
 - 13: sp_vertebrate:*
 - 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5019	100.0	915	4 Q13827	Q13827 homo sapien
2	4681	93.3	863	4 Q13822	Q13822 homo sapien
3	4666	93.0	863	4 Q15117	Q15117 homo sapien
4	4439.5	88.5	862	11 Q9RIE6	Q9RIE6 mus musculus
5	4306	85.8	885	11 Q64610	Q64610 rattus norv
6	2084	41.5	875	11 Q63490	Q63490 rattus norv
7	2084	41.5	875	11 P97676	P97676 rattus norv
8	2081	41.5	875	11 P97675	P97675 rattus norv
9	2057.5	41.0	876	11 P70641	P70641 rattus norv
10	2040.5	40.7	875	4 Q14638	Q14638 homo sapien
11	1955.5	39.0	845	4 Q9NP23	Q9NP23 homo sapien
12	1955.5	39.0	925	4 Q9PIP6	Q9PIP6 homo sapien
13	1151	22.9	817	14 Q90761	Q90761 fowlpox vir
14	1151	22.9	817	14 Q905H1	Q905H1 fowlpox vir
15	646.5	12.9	457	10 Q9S082	Q9S082 arabidopsis
16	613	12.2	479	10 Q9FS13	Q9FS13 spinacia ol
17	612	12.2	496	10 Q9S083	Q9S083 arabidopsis
18	611.5	12.2	479	10 Q42974	Q42974 oryza sativ
19	610	12.2	829	5 P90754	P90754 caenorhabdi

20	609	12.1	461	10 Q9S081	Q9S081 arabidopsis
21	539.5	10.7	485	3 Q94323	Q94323 schizosacch
22	534	10.6	251	4 Q9NQW9	Q9NQW9 homo sapien
23	526.5	10.5	257	11 O88827	O88827 rattus norv
24	522	10.4	429	2 O69013	O69013 zymomonas m
25	512	10.2	453	4 Q9Y6X5	Q9Y6X5 homo sapien
26	474.5	9.5	477	11 Q9EQG7	Q9EQG7 mus musculu
27	466.5	9.3	477	4 Q9UJAG	Q9UJAG homo sapien
28	461	9.2	433	2 Q9PAB9	Q9PAB9 xylella fas
29	456.5	9.1	674	5 P90755	P90755 caenorhabdi
30	427	8.5	152	4 Q9H515	Q9H515 homo sapien
31	394.5	7.9	281	6 Q9TSB2	Q9TSB2 bos taurus
32	309.5	6.2	151	11 Q9QYV2	Q9QYV2 rattus norv
33	297.5	5.9	614	5 Q17540	Q17540 caenorhabdi
34	241.5	4.8	133	10 Q9S080	Q9S080 arabidopsis
35	238	4.7	453	5 Q22129	Q22129 caenorhabdi
36	234	4.7	45	4 Q14555	Q14555 homo sapien
37	171	3.4	385	13 Q9PTU6	Q9PTU6 paralichthy
38	170.5	3.4	44	11 Q9RI15	Q9RI15 mus musculu
39	163	3.2	360	5 O45359	O45359 caenorhabdi
40	158.5	3.2	1054	11 Q9JM99	Q9JM99 mus musculu
41	145.5	2.9	465	2 O69954	O69954 streptomyce
42	142	2.8	1186	14 O55767	O55767 chilo iride
43	135	2.7	32	6 Q9TRD2	Q9TRD2 bos taurus
44	134	2.7	1404	4 Q92954	Q92954 homo sapien
45	132	2.6	462	2 Q9Z4Z4	Q9Z4Z4 streptomyce

ALIGNMENTS

RESULT	1				
Q13827					
ID	Q13827	PRELIMINARY;	PRT;	915 AA.	
AC	Q13827;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)				
DE	AUTOTAXIN.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=TUMOR;				
RX	MEDLINE=95074054; PubMed=7982964;				
RA	Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A.,				
RA	Sobel M.E., Liotta L.A., Stracke M.L.;				
RT	"cDNA cloning of the human tumor motility-stimulating protein,				
RT	autotaxin, reveals a homology with phosphodiesterases.";				
RL	J. Biol. Chem. 269:30479-30484(1994).				
DR	EMBL; L35594; AAA64785.1;				
DR	InterPro: IPR001212;				
DR	InterPro: IPR001604;				
DR	InterPro: IPR002591;				
DR	Pfam: PF01033; Somatomedin_B; 2.				
DR	Pfam: PF01663; Phosphodiester; 1.				
DR	PRINTS; PR00022; SOMATOMEDINB.				
DR	PROSITE; PS00524; SOMATOMEDIN_B; 2.				
DR	SMART; SM00477; NUC; 1.				
SQ	SEQUENCE 915 AA; 105246 MW; 2BE6135CCD837780 CRC64;				

Query Match	100.0%;	Score	5019;	DB	4;	Length	915;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	915;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	MARRSFQSQIISLFTFAVGVSGICLGTFAHRIKRAEGWEGPPTVLSDSPWTNISGCK	60				
DB	1	MARRSFQSQIISLFTFAVGVSGICLGTFAHRIKRAEGWEGPPTVLSDSPWTNISGCK	60				
QY	61	GRCFELQEAQPPDCNLCNKSYTSCCHDFELCLTKARGWECTKRCGEVRNEENACHC	120				


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Db 61 GRCFELQAGPPDCRDLNCKSYTSCCHDFELCLKTARGWECTKRCGEVNRNEENACHC 120
QY 121 SEDCLARGDCCTNYQVCKGESHVDDCEBEIKAAECGAGVVRPPLIIFSVGDFRASYMK 180
Db 121 SEDCLARGDCCTNYQVCKGESHVDDCEBEIKAAECGAGVVRPPLIIFSVGDFRASYMK 180
QY 181 KGSVMPNIEKLSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMDVPVDA 240
Db 181 KGSVMPNIEKLSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMDVPVDA 240
QY 241 TFHLRGREKFNHRWGGQPLWITATKQVKGAGTFWVSWVIPHERRILTLRLWTLDPDHER 300
Db 241 TFHLRGREKFNHRWGGQPLWITATKQVKGAGTFWVSWVIPHERRILTLRLWTLDPDHER 300
QY 301 PSVYAFYSEQPDFSGHKYGGPPESSVSGSPETPAKRPKRKRVAPKRRR 360
Db 301 PSVYAFYSEQPDFSGHKYGGPPESSVSGSPETPAKRPKRKRVAPKRRR 360
QY 361 KIHRMDHYAAETRODKMTNPLREIDKIVGQMDGLKQLKRRVCNVIFVGDHGMEDVTC 420
Db 361 KIHRMDHYAAETRODKMTNPLREIDKIVGQMDGLKQLKRRVCNVIFVGDHGMEDVTC 420
QY 421 RTEPLSNLTVNDDITLVPGTLGRIRSKFSNNAKYDPKAIITANLTCKPDQHFYKPKQH 480
Db 421 RTEPLSNLTVNDDITLVPGTLGRIRSKFSNNAKYDPKAIITANLTCKPDQHFYKPKQH 480
QY 481 LPKRLHYANNRRIEDIHLVRRHWHVARKPLDVYKPSGKCFQGDHGDGNKNSMQTVF 540
Db 481 LPKRLHYANNRRIEDIHLVRRHWHVARKPLDVYKPSGKCFQGDHGDGNKNSMQTVF 540
QY 541 VGYGPTFKYTKVPPFENIELYNVMDLLGLKAPNNGTHGSLNHLRTNFRPTMPPEV 600
Db 541 VGYGPTFKYTKVPPFENIELYNVMDLLGLKAPNNGTHGSLNHLRTNFRPTMPPEV 600
QY 601 TRPNYGMYLQSDFDLGCTCDDKVEPKNKLDLNLKRLHGTGSTEERHLLYGRPAVLRYT 660
Db 601 TRPNYGMYLQSDFDLGCTCDDKVEPKNKLDLNLKRLHGTGSTEERHLLYGRPAVLRYT 660
QY 661 RYDILYTHDFESGSEIFLMULWTSYTVSKQAEVSSVDPDLTSCVRPDRVSPFSQNC 720
Db 661 RYDILYTHDFESGSEIFLMULWTSYTVSKQAEVSSVDPDLTSCVRPDRVSPFSQNC 720
QY 721 AYKNDKQMSYGFLEPPYLSLSSPEAKYDAFLTNMVMYPAFKRVWNYVQFVLVKKYASER 780
Db 721 AYKNDKQMSYGFLEPPYLSLSSPEAKYDAFLTNMVMYPAFKRVWNYVQFVLVKKYASER 780
QY 781 NGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVPHYYSIITSCLDFTQPADKCDGP 840
Db 781 NGVNVISGPIFDYDGLHDTEDKIKQYVEGSSIPVPHYYSIITSCLDFTQPADKCDGP 840
QY 841 LSVSSFLPHRPNDESCNSEDSESKVVEELMKMHTARVRDIEHLTSLDFRKTSSRYPE 900
Db 841 LSVSSFLPHRPNDESCNSEDSESKVVEELMKMHTARVRDIEHLTSLDFRKTSSRYPE 900
QY 901 ILTLKTYLHYESEI 915
Db 901 ILTLKTYLHYESEI 915
```

RESULT 2

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Q13822 PRELIMINARY; PRT; 863 AA.
AC Q13822;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE AUTOTAXIN-T.
GN ATX-T.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RN RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Murata J., Lee H.Y., Clair T., Kruttsch H.C., Arestad A.A.,
RA Sobel M.E., Liotta L.A., Stracke M.L.;
RT "cDNA cloning of the human tumor motility-stimulating protein,
RL autotaxin, reveals a homology with phosphodiesterases.";
RN J. Biol. Chem. 269:30479-30484(1994).
[2]
RN RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=96158950; PubMed=8579579;
RA Lee H.Y., Murata J., Clair T., Polymeropoulos M.H., Torres R.,
RA Manrow R.E., Liotta L.A., Stracke M.L.;
RT "Cloning, chromosomal localization, and tissue expression of autotaxin
RL from human teratocarcinoma cells.";
DR EMBL; L46720; AA000855.1; -.
DR InterPro; IPR001212; -.
DR InterPro; IPR001604; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiester; 1.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 863 AA; 99017 MW; F960DCE51663BABC CRC64;
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Query Match 93.3%; Score 4681; DB 4; Length 863;

Best Local Similarity 93.8%; Pred. No. 0;

Matches 858; Conservative 2; Mismatches 3; Indels 52; Gaps 1;

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QY 1 MARRSFQSCQIISLFTFAVGYSICLGFTHAHRKRAEGWEEGPTVLSDSPWNTNIGSCK 60
Db 1 MARRSFQSCQIISLFTFAVGYNICLGFTHAHRKRAEGWEEGPTVLSDSPWNTNIGSCK 60
QY 61 GRCFELQAGPPDCRDLNCKSYTSCCHDFELCLKTARGWECTKRCGEVNRNEENACHC 120
Db 61 GRCFELQAGPPDCRDLNCKSYTSCCHDFELCLKTARGWECTKRCGEVNRNEENACHC 120
QY 121 SEDCLARGDCCTNYQVCKGESHVDDCEBEIKAAECGAGVVRPPLIIFSVGDFRASYMK 180
Db 121 SEDCLARGDCCTNYQVCKGESHVDDCEBEIKAAECGAGVVRPPLIIFSVGDFRASYMK 180
QY 181 KGSVMPNIEKLSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMDVPVDA 240
Db 181 KGSVMPNIEKLSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMDVPVDA 240
QY 241 TFHLRGREKFNHRWGGQPLWITATKQVKGAGTFWVSWVIPHERRILTLRLWTLDPDHER 300
Db 241 TFHLRGREKFNHRWGGQPLWITATKQVKGAGTFWVSWVIPHERRILTLRLWTLDPDHER 300
QY 301 PSVYAFYSEQPDFSGHKYGGPPESSVSGSPETPAKRPKRKRVAPKRRR 360
Db 301 PSVYAFYSEQPDFSGHKYGGPPESSVSGSPETPAKRPKRKRVAPKRRR 360
QY 361 KIHRMDHYAAETRODKMTNPLREIDKIVGQMDGLKQLKRRVCNVIFVGDHGMEDVTC 420
Db 361 KIHRMDHYAAETRODKMTNPLREIDKIVGQMDGLKQLKRRVCNVIFVGDHGMEDVTC 420
QY 421 RTEPLSNLTVNDDITLVPGTLGRIRSKFSNNAKYDPKAIITANLTCKPDQHFYKPKQH 480
Db 421 RTEPLSNLTVNDDITLVPGTLGRIRSKFSNNAKYDPKAIITANLTCKPDQHFYKPKQH 480
QY 481 LPKRLHYANNRRIEDIHLVRRHWHVARKPLDVYKPSGKCFQGDHGDGNKNSMQTVF 540
Db 481 LPKRLHYANNRRIEDIHLVRRHWHVARKPLDVYKPSGKCFQGDHGDGNKNSMQTVF 540
QY 541 VGYGPTFKYTKVPPFENIELYNVMDLLGLKAPNNGTHGSLNHLRTNFRPTMPPEV 600
Db 541 VGYGPTFKYTKVPPFENIELYNVMDLLGLKAPNNGTHGSLNHLRTNFRPTMPPEV 600
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QY 601 TRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDELNKLRLHTKGTSTERHLLYGRPAVLRYT 660
DB 549 TRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDELNKLRLHTKGTSTERHLLYGRPAVLRYT 608
QY 661 RYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDRVRSFSQNC 720
DB 609 RYDILYHTDFESGYSEIFLMLPLWTSYTVSKQAEVSSVPDHLTSCVRPDRVRSFSQNC 668
QY 721 AYKNDKQMSYGLFPPYLSLSSPEAKYDAFLVTNMVPMYPAFKRVWNYFORVLYKKYASER 780
DB 669 AYKNDKQMSYGLFPPYLSLSSPEAKYDAFLVTNMVPMYPAFKRVWNYFORVLYKKYASER 728
QY 781 NGVNVISGPIFYDYGDLHDTEDKIQYVEGSSIPVPTHYISITSCLDFTQPADKCDGP 840
DB 729 NGVNVISGPIFYDYGDLHDTEDKIQYVEGSSIPVPTHYISITSCLDFTQPADKCDGP 788
QY 841 LSVSSFILPHRPDNEESCNSDESKWVEELMKMHTARVDIEHLTSLDFFRKTSSYPE 900
DB 789 LSVSSFILPHRPDNEESCNSDESKWVEELMKMHTARVDIEHLTSLDFFRKTSSYPE 848
QY 901 ILTLKTYLHTYSEI 915
DB 849 ILTLKTYLHTYSEI 863

RESULT 3
Q15117 ID Q15117 PRELIMINARY; PRT; 863 AA.
AC Q15117;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE PHOSPHODIESTERASE I ALPHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163899; PubMed=8586446;
RA Kawagoe H., Soma O., Goji J., Nishimura N., Narita M., Inazawa J.,
RA Nakamura H., Sano K.;
RT "Molecular cloning and chromosomal assignment of the human brain-type
RT phosphodiesterase I/nucleotide pyrophosphatase gene (PDNP2).";
RL Genomics 30:380-384 (1995).
DR EMBL; D45421; BAA08260.1; -
DR InterPro; IPR001212; -
DR InterPro; IPR001604; -
DR InterPro; IPR002591; -
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiester_1.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 863 AA; 99040 MW; 318EA28BICEA7A55 CRC64;

Query Match 93.0%; Score 4666; DB 4; Length 863;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 855; Conservative 3; Mismatches 5; Indels 52; Gaps 1;

QY 1 MARRSFSQCIISLFTFVAVGVCISLGFTHAKRAEGWEGPPTVLSDPWNTNIGSGCK 60
DB 1 MARRSFSQCIISLFTFVAVGVCISLGFTHAKRAEGWEGPPTVLSDPWNTNIGSGCK 60
QY 61 GRCFELQAGPPDCRDNLCYSKTSCHDFDELCLKTARGWECTKRCGEVRNEENACHC 120
DB 61 GRCFELQAGPPHCRDNLCYSKTSCHDFDELCLKTARGWECTKRCGEVRNEENACHC 120
QY 121 SEDCLARGDCCTNYQVCKGESHVDDDCETKAAECAPAGVRPPLIIFSVDFRASYMK 180
DB 121 SEDCLARGDCCTNYQVCKGESHVDDDCETKAAECAPAGVRPPLIIFSVDFRASYMK 180
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QY 181 KSKVMPNIEKLRSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMDPVFDA 240
DB 181 KSKVMPNIEKLRSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMDPVFDA 240
QY 241 TFHLRGREKFNHRWGGOPWLITATKQGVKAGTFWSSVVIPIHERRILTLRLWLPDHER 300
DB 241 TFHLRGREKFNHRWGGOPWLITATKQGVKAGTFWSSVVIPIHERRILTLRLWLPDHER 300
QY 301 PSYAFYSEQPDFSGHKYGPPESSYSGSFPTAKRPRKVAAPKRQERPAPPKRRR 360
DB 301 PSYAFYSEQPDFSGHKYGPPE----- 324
QY 361 KIRHMDYAAETRODKQTNPLREIDKIVGQMDGLKQLKRRCVNIFVGDHGMEDVTC 420
DB 325 -----MTNPLREIDKIVGQMDGLKQLKRRCVNIFVGDHGMEDVTC 368
QY 421 RTEFLSNLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIITANLTCKKPDQHFPLYKQH 480
DB 369 RTEFLSNLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIITANLTCKKPDQHFPLYKQH 428
QY 481 LPKRLHYANNRRRIEDIHLLVERRHVARKPLDYVKKPSGCKFFQGDHGFNDKVNMQTVF 540
DB 429 LPKRLHYANNRRRIEDIHLLVERRHVARKPLDYVKKPSGCKFFQGDHGFNDKVNMQTVF 488
QY 541 VGYPTEFKYTKVPPFENIELYNVMDLLGLKPAIPNNNGTHGSLNHLRTNTFRPTMPEV 600
DB 489 VGYPTEFKYTKVPPFENIELYNVMDLLGLKPAIPNNNGTHGSLNHLRTNTFRPTMPEV 548
QY 601 TRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDELNKLRLHTKGTSTERHLLYGRPAVLRYT 660
DB 549 TRPNYPGIMYLSQDFDLGCTCDDKVEPKNKLDELNKLRLHTKGTSTERHLLYGRPAVLRYT 608
QY 661 RYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDRVRSFSQNC 720
DB 609 RYDILYHTDFESGYSEIFLMLPLWTSYTVSKQAEVSRVPDHLTSCVRPDRVRSFSQNC 668
QY 721 AYKNDKQMSYGLFPPYLSLSSPEAKYDAFLVTNMVPMYPAFKRVWNYFORVLYKKYASER 780
DB 669 AYKNDKQMSYGLFPPYLSLSSPEAKYDAFLVTNMVPMYPAFKRVWNYFORVLYKKYASER 728
QY 781 NGVNVISGPIFYDYGDLHDTEDKIQYVEGSSIPVPTHYISITSCLDFTQPADKCDGP 840
DB 729 NGVNVISGPIFYDYGDLHDTEDKIQYVEGSSIPVPTHYISITSCLDFTQPADKCDGP 788
QY 841 LSVSSFILPHRPDNEESCNSDESKWVEELMKMHTARVDIEHLTSLDFFRKTSSYPE 900
DB 789 LSVSSFILPHRPDNEESCNSDESKWVEELMKMHTARVDIEHLTSLDFFRKTSSYPE 848
QY 901 ILTLKTYLHTYSEI 915
DB 849 ILTLKTYLHTYSEI 863

RESULT 4
Q9RLB6 ID Q9RLB6 PRELIMINARY; PRT; 862 AA.
AC Q9RLB6;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE (EC 3.1.4.1).
GN NPPS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57B/6;
RA Sano K., Piao J.-H.;
RT "Cloning and chromosomal assignment of mouse phosphodiesterase
RT I/nucleotide pyrophosphatase (pd-I alpha/autotaxin).";
```

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF123542; AAD46480.1; -
DR InterPro: IPR001212; -
DR InterPro: IPR002591; -
DR Pfam: PF01033; Somatomedin_B; 2.
DR Pfam: PF01663; Phosphodiester; 1.
DR PRINTS: PR00022; SOMATOMEDINB.
DR PROSITE: PS00524; SOMATOMEDIN_B; 2.
DR SMART: SM00201; SO; 1.
KW Hydrolase.
SQ SEQUENCE 862 AA; 98918 MW; 641F8F1443E4F8B0 CRC64;

Query Match 88.5%; Score 4439.5; DB 11; Length 862;
Best Local Similarity 88.1%; Pred. No. 0;
Matches 806; Conservative 30; Mismatches 26; Indels 53; Gaps 2;

QY 1 MARRSFQSQIISLFTFAGVSGICLGTATRIKRAEGWEGPPVILSDSPWNTSGSK 60
Db 1 MARGCGFSGYQVISLFTFAIGVNLCLGFTASRIKRAE-WDEGPTVLSDSPWNTSGSK 59
QY 61 GRCELEQAGPPDCRDNLCYSKSCCHDFELCLKTARGWECTKDRGGEVNEENACHC 120
Db 60 GRCELEQAGPPDCRDNLCYSKSCCHDFELCLKTARGWECTKDRGGEVNEENACHC 119
QY 121 SEDCLARGDCCNTQVVCCKGSHWDDCEIEIKAAECFAGFVRPPLIIFSVGDFRASYMK 180
Db 120 SEDCLRGDCCNTQVVCCKGSHWDDCEIEIRVECFAGFVRPPLIIFSVGDFRASYMK 179
QY 181 KGSVMPNIEKLRCGTHSPYMRPVYPTKTPNLTATGLYPESHGIVGNSMYDPVFA 240
Db 180 KGSVMPNIEKLRCGTHSPYMRPVYPTKTPNLTATGLYPESHGIVGNSMYDPVFA 239
QY 241 TFHLRGREKFNHRWGGPPLITATKQGVKAGTFVSWVIPHERILILRLWLTLPDHER 300
Db 240 TFHLRGREKFNHRWGGPPLITATKQGVKAGTFVSWVIPHERILILRLWLTLPDHER 299
QY 301 PSVAFYSEQDFSGHKYGPFGPESSYSGSPPTPAKRKRKVPAPKRQRPVAPPKRRR 360
Db 300 PSVAFYSEQDFSGHKYGPFGPE----- 323
QY 361 KIHMDHYAAETRODKMTNPRLREIDKIVGQMDGLKQLKLRRCVNVIFVGDHGMEDVTCD 420
Db 324 -----MTNPLREIDKTVGQMDGLKQLKLRRCVNVIFVGDHGMEDVTCD 367
QY 421 RTEFLSNLTWDDITVPGILGRTRSFNSNAKYDPAKAIANLTKCPDQHFYKYLKH 480
Db 368 RTEFLSNLTWDDITVPGILGRIRPKIPNNLYDKPAITANLTKCPDQHFYKYLKH 427
QY 481 LPKRLHYANNRRIEDIHLLVERRHVARKPLDYKKPSGCKCFQGDHGFNDKVNMQTVF 540
Db 428 LPKRLHYANNRRIEDHLVRRHVARKPLDYKKPSGCKCFQGDHGFNDKVNMQTVF 487
QY 541 VGYGPTFKYTKVPPFENIELYNVCMDDLGLKAPNNGTHGSLNHLRLTNTFRPTMPREV 600
Db 488 VGYGPTFKYTKVPPFENIELYNVCMDDLGLKAPNNGTHGSLNHLRLTNTFRPTLPREV 547
QY 601 TRPNPTGMYLQSDFDLCTCDDKVEPKNKLDELNKLHKTGSTERHLLYGRPAVLYRT 560
Db 548 SRTNPTGMYLQSDFDLCTCDDKVKPNKLEELNKLHKTGSTERHLLYGRPAVLYRT 607
QY 661 RYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRRPVRVSPFSQNC 720
Db 608 SYDILYHTDFESGYSEIFLMLWTSYTVSKQAEVSSIFELHLLTNCVRRPVRVSPFSQNC 667
QY 721 AYKNDKQMSYGLFPPYLLSSPEAKYDAFLVTNMVPMYPAKRVVNYFQRLVVKYASER 780
Db 668 AYKNDKQMSYGLFPPYLLSSPEAKYDAFLVTNMVPMYPAKRVVNYFQRLVVKYASER 727
QY 781 NGVNVISGPIFDYDGLHDEDKTKQVVEGSSIPVPHYYSIIITSCLDFTPADKCDGP 840
Db 728 NGVNVISGPIFDYNYGLRDIEDEIKQVVEGSSIPVPHYYSIIITSCLDFTPADKCDGP 787

QY 841 LSVSSFILPHRPDNEBSCNSEDSEKWKVLELKMHTARVDRDIEHLTSLDFFKTSRYSPE 900
Db 788 LSVSSFILPHRPDNEBSCNSEDSEKWKVLELKMHTARVDRDIEHLTGLDIFYRKTYSYSE 847
QY 901 ILTLKTYLHTYSEI 915
Db 848 ILTLKTYLHTYSEI 862
RESULT 5
Q64610 PRELIMINARY; PRT; 885 AA.
AC Q64610;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE PHOSPHODIESTERASE I (EC 3.1.4.1).
GN NPH-TYPE III.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLIN=95050605; PubMed=7961762;
RA Narita M., Goji J., Nakamura H., Sano K.;
RT "Molecular cloning, expression, and localization of a brain-specific
phosphodiesterase I/nucleotide pyrophosphatase (PD-I alpha) from rat
brain";
RL J. Biol. Chem. 269:28235-28242(1994).
DR EMBL: D28560; BAA05910.1; -
DR InterPro: IPR001212; -
DR InterPro: IPR001604; -
DR InterPro: IPR002591; -
DR Pfam: PF01033; Somatomedin_B; 2.
DR Pfam: PF01663; Phosphodiester; 1.
DR PRINTS: PR00022; SOMATOMEDINB.
DR PROSITE: PS00524; SOMATOMEDIN_B; 2.
DR SMART: SM00477; NUC; 1.
KW Hydrolase.
SQ SEQUENCE 885 AA; 101309 MW; 8C5C0AFC52007973 CRC64;

Query Match 85.8%; Score 4306; DB 11; Length 885;
Best Local Similarity 83.6%; Pred. No. 0;
Matches 792; Conservative 33; Mismatches 28; Indels 94; Gaps 6;

QY 1 MARRSFQSQIISLFTFAGVSGICLGTATRIKRAEGWEGPPVILSDSPWNTSGSK 60
Db 1 MARGCGFSGYQVISLFTFAIGVNLCLGFTASRIKRAE-WDEGPTVLSDSPWNTSGSK 59
QY 61 GRCELEQAGPPDCRDNLCYSKSCCHDFELCLKTARGWECTKDRGGEVNEENACHC 120
Db 60 GRCELEQAGPPDCRDNLCYSKSCCHDFELCLKTARGWECTKDRGGEVNEENACHC 119
QY 121 SEDCLARGDCCNTQVVCCKGSHWDD-----DCEIEIKAAECFAGFVRPPLIIFSVDG 173
Db 120 PEDCLRGDCCNTQVVCCKGSHWDDAARNQSECLQV-----CP-----PPLIIFSVDG 170
QY 174 FRASYMKKSKVMPNIEKLRCGTHSPYMRPVYPTKTPNLTATGLYPESHGIVGNSM 233
Db 171 FRASYMKKSKVMPNIEKLRCGTHSPYMRPVYPTKTPNLTATGLYPESHGIVGNSM 230
QY 234 YDVFDAETHLRGKFNHRWGGQPLWITATKQGVKAGTFVSWVIPHERILILRLW 293
Db 231 YDVFDAETHLRGKFNHRWGGQPLWITATKQGVKAGTFVSWVIPHERILILRLW 290
QY 294 TLPDHERPSVYAEYSEOPDFSGHKYGPFGPESSYSGSPPTPAKRKRKVPAPKRQRPVA 353
Db 291 SLDPNERPSVYAEYSEOPDFSGHKYGPFGPE----- 321
QY 354 PPKRRRRKTHRMDHYAAETRODKMTNPRLREIDKIVGQMDGLKQLKLRRCVNVIFVGDH 413

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Db 322 -----MTNPLREIDKTVGQMDGLKQLLRHCNVVIFVGDHG 358
Qy 414 MEDVTCDRTEFLSNLTNVDITLVPGLTGRTRSKFSNNAKYDPKAIANLTKCKPDQHF 473
Db 359 MEDVTCDRTEFLSNLTNVDITLVPGLTGRTRAKSINKSKYDPKIIANLTKCKPDQHF 418
Qy 474 KPYLKQHLPLKRLHYANNRRIEDIHLVRRWHVARKPLDVKYKPSKCFQFGDGHFNKV 533
Db 419 KPYMKQHLPLKRLHYANNRRIEDIHLVDRWHVARKPLDVKYKPSKCFQFGDGHFNKV 478
Qy 534 NSMQTVFVGYGPTFKYKTKVPFFENIELYNVACDLGLKAPAPNNGTHGSLNHLRLTNTFR 593
Db 479 NSMQTVFVGYGPTFKYKTKVPFFENIELYNVACDLGLKAPAPNNGTHGSLNHLRLTNTFR 538
Qy 594 PTMPEVTRPNYPGIMYLSQSDLGCTCDKDKPEKPKNKLDELANKRLHTKSGTE----- 645
Db 539 PTMPEVSRPNYPGIMYLSQSDLGCTCDKDKPEKPKNKLDELANKRLHTKSGTEAETGKFRG 598
Qy 646 -----ERHLLYGRPAVLRYTRIDILYHTDFESGYSEIFLMLLTYSYTV 688
Db 599 SKHENKKNLINGSVEPKERHLLYGRPAVLRYTRIDILYHTDFESGYSEIFLMPLWTSYTI 658
Qy 689 SKQAEVSSVPDHLTSCVRPDRVSPFSQNCILAYKNDKQMSYGFLLPPLSSSPEAKYDA 748
Db 659 SKQAEVSSIPPEHLTNCVRPDRVSPFSQNCILAYKNDKQMSYGFLLPPLSSSPEAKYDA 718
Qy 749 FLVTNNVPMYPAFKRWYVQFVLYVKKYASERNVNVISGPIFDYDGLHDTEDIKQY 808
Db 719 FLVTNNVPMYPAFKRWYVQFVLYVKKYASERNVNVISGPIFDYDGLHDTEDIKQY 778
Qy 809 VEGGSIPVPTHYISITSCDFTQADKCDGPLSVSSFILPHRPDNEESCNSEDESKWV 868
Db 779 VEGGSIPVPTHYISITSCDFTQADKCDGPLSVSSFILPHRPDNEESCNSEDESKWV 838
Qy 869 BELMKMHTARVARDIEHLTSLDFRKTSSYPBELTLTKTLTYLHYESEI 915
Db 839 BELMKMHTARVARDIEHLTSLDFRKTSSYPBELTLTKTLTYLHYESEI 885

RESULT 6
Q63490 PRELIMINARY; PRT; 875 AA.
AC Q63490;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE RB13-6 ANTIGEN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAQUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE=95247775; PubMed=7730366;
RA Deissler H., Lottspeich F., Rajewsky M.F.;
RT "Affinity purification and cDNA cloning of rat neural differentiation
RT and tumor cell surface antigen gp130RB13-6 reveals relationship to
RT human and murine PC-1."
RL J. Biol. Chem. 270:9849-9855(1995).
DR EMBL; Z47987; CAA88029.1; -.
DR InterPro; IPR001212; -.
DR InterPro; IPR001604; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiester_1.
DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 875 AA; 99087 MW; 9BA9BF82DFA6 CRC64;
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Query Match 41.5%; Score 2084; DB 11; Length 875;

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Best Local Similarity 43.5%; Pred. No. 9.6e-162;
Matches 386; Conservative 160; Mismatches 248; Indels 94; Gaps 11;

Qy 57 GSCRGRCFELQEAQPPCCDNLCKSVTSCCHDDELCLKTARGWECKDRGGEVRNEEN 116
Db 53 GSCRRKCFDSSHRGLEGRCDSCGCTDRGDCWDFEDTCVKSTQIWTCSFRGGETRLEAA 112
Qy 117 ACHSEBCLARGDCCTNYQVYCKGSHWVDDCEBEIKAAECAPAGVRPPLIIFSVDGFA 176
Db 113 LCSCADCLQRKDCCTDYKAVCQGEVPMWTEACASSQPQCEGFDQPPVILFSDMGFA 172
Qy 177 SYMKGSKVMPNIEKLSCGTHSPYMRPVYTKTPNPLYTLATGLYPESHGIVGNSWDP 236
Db 173 EYLQWSTLLPNINKLTCGLHSHKYMRYMPTKTPNHYITVTGLYPESHGIIDNNMYDV 232
Qy 237 VFDATEHLRGKEKHNHMGQPLWITATKOGVKGATFFW-----SV 278
Db 233 YLNKNFVSSVSSKSNPAWMSGQPLWTAMYQLKAAASYILGSDVAVNGSPNPIYRNSN 292
Qy 279 VIPHERILTLRWLTLPDHERPSVYAFYSQPDPSFGHKYGFPGPESSYSGSPFPAKRP 338
Db 293 SVPYESRIATLLQWLDLPKAERPSTFYIYVEEPSAGHSGPV-----SAG----- 338
Qy 339 KRKVAPKRQERPVPAPPKRRKRKTHRMDHYAAETRQDKMTNPLREIDKIVGQMDGLKQL 398
Db 339 -----VIKALQLVDDAFGLMBGLKQR 360
Qy 399 KLRCVNVIFVGDHGMEDVTCDRTEFLSNLTNVDITLVPGLTGRIRSK-----FSNN 452
Db 361 NLHNCVNIIVLADHGMQDTSQDRVEYMTDYFPEI-NFYMYQGAPAPRIETRIPODFTFN 419
Qy 453 AKYDPKAIANLTKCKPDQHFVKYLKQHLPKRLHYANNRRIEDIHLVRRWHVARKPLD 512
Db 420 S-----EELVRDLSCRSKSDQHFKPYLTDLPLKRLHYAKNVRIDKVLHVDROWLAYR----- 471
Qy 513 VYKPSGKCFQFGDGHFNKVNMSQTVFVGYGPTFKYKTKVPFFENIELYNVACDLGLK 572
Db 472 --NKGSSNC-EGGTHGYNNEFKSMEATFLAHGSPFKEKTVIEPENIEVYNLCDDLHIQ 528
Qy 573 PAPNNGTHGSLNHLRLTNTFRPTMPPEVTRPNYPGIMYLSQSDLGCTCDKDKVEPKNKL 632
Db 529 PAPNNGSHGSLNHLKAPFYQPSHAEISLSAGCGFTTLPKDSLNCSC-LALQTSQGE 587
Qy 633 ELNKLRLTKG-----STEERHLLYGRPAVLRYTR-YDILYHTDFESGYSEIFLMLLTYSY 687
Db 588 QVNORLNLSGEVSATEKTNLPFRPRVIOKNKDCHLLYHREYVSGFGKAMKMPWSSIT 647
Qy 688 VSKQAEVSSVPDHLTSCVRPDRVSPFSQNCILAYKNDKQMSYGFLLPPLSSSPEAKYD 747
Db 648 VPKPGDTSSLPTVPCLRADRVDPSESKCSFYLADQNDHGLYPPAIIKGNESQYD 707
Qy 748 AFLVTNNVPMYPAFKRWYVQFVLYVKKYASERNVNVISGPIFDYDGLHDTEDIKQ 807
Db 708 ALITSLNLPVPMYKEFKMWDYFHKVLLIKYATERGNVNVISGPIFDYDGLHDTEDITN 767
Qy 808 YVEGSSIPVPTHYISITSCDFTQADKCDGPLSVSSFILPHRPDNEESCNSEDESKW 867
Db 768 YVAGTDVPTVPTHYISITSCDFTQADKCDGPLSVSSFILPHRPDNEESCNSEDESKW 827
Qy 868 VEELMKMHTARVARDIEHLTSLDFRKTSSYPBELTLTKTLTYLHYESEI 915
Db 828 VEERFKAHARVDRVELLTGLDFYQEKTPQVSEILQLKTLPTETII 875

RESULT 7
P97676
ID P97676 PRELIMINARY; PRT; 875 AA.
AC P97676;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ALKALINE PHOSPHODIESTERASE.
OS Rattus norvegicus (Rat).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97250927; PubMed=9096610;
RA Scott L.J., Delautier D., Meerson N.R., Trugnan G., Goding J.W.,
RA Maurice M.;
RT "Biochemical and molecular identification of distinct forms of
RT alkaline phosphodiesterase I expressed on the apical and basolateral
RT plasma membrane surfaces of rat hepatocytes.";
RL Hepatology 25:995-1002(1997).
DR EMBL; U78788; AAB61536.1; -;
DR InterPro; IPR001212; -;
DR Pfam; PF01663; Phosphodiesterase; 1.
DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART; SM00201; SO; 1.
SQ SEQUENCE 875 AA; 99071 MW; 4205F263E8A933EA CRC64;

Query Match 41.5%; Score 2084; DB 11; Length 875;
Best Local Similarity 43.5%; Pred. No. 9.6e-162;
Matches 386; Conservative 160; Mismatches 248; Indels 94; Gaps 11;

QY 57 GSKGRCFELQAGPPDCRCDNLCKSVTSCCHDFDELCLKTARGWECTKRCGGEVRNEEN 116
DB 53 GSKKKCFDSHRLGECRCDSGCTDRGCCDWDFETCVKSTQIWTCSNFRCEGTRLEAA 112
QY 117 ACHGSEDCLAGDCCTNYQVVKCGESHVDDDCDEEIKAAECAGFVRPLLIIFSVDGFA 176
DB 113 LSCADDCLOKDCCTDYKAVCQGEVPMWTEACASSQEPQCEGDPVVLFSMDGFA 172
QY 177 SYMKKSKVMPNIEKLKSCGTHSPYMPVPTKTPNLYTLATGLYPESHGIVGNSMDP 236
DB 173 EYLQWSTLLPNINKLTKCGLHSHKYMRAVYPTKTPFNHYTIVTGLYPESHGIIIDNNM 232
QY 237 VFDTATHLRGREKFNHWWGQPLWITATKQGVKAGTFW; - - - - -SV 278
DB 233 YLNKNFSLSSVEKSNPAWWSGQPIWLMTAMYGOLKAAASHYWPSCDVAVNGSPFNIRNYSN 292
QY 279 VIPHERILATLRLWLTLPDHERPSVAFYSEQDPFSGHKYGFPGPEESYSGSPFTPAKRP 338
DB 293 SVPTESRIATLLQWLDLPKAERPFYTIYVEEPPDSAGHSGPV; - - - - -SAG 338
QY 339 KRKVAPKRROERPVPAPPKRRRKTHRMHDYAAETRODKMTNPLREIDKIVGOLMDGLKOL 398
DB 339 - - - - -VIRALQLVDDAFGLMEGLKQR 360
QY 399 KLRGVNVIFVGDHGMEDVTCRTEFLSNLYLTNVDDIYLVPGTLGRISK; - - - - -FSNN 452
DB 361 NLHNCVNIIVLADHGMQDQTSRDEYMTDYPPEI - NFMYOGAPAPRIARTNPQDFFTN 419
QY 453 AKYDPKAIANTLCKPDQHPKLYKHLPRKLVANNRRIEDILLVBRVHWARKPLD 512
DB 420 S - - - - -EELVRLDCKSKSDQHPKPLTPDLPRLHYAKVNRIDKVLHWDRLQWLAR - - - - -471
QY 513 VYKPSGKCFQGDHGFNDKYNMQTVFVGYGPTFKYKTKVPPFENIELYNMCDLLGLK 572
DB 472 - - - - -NGSSNC - EGGTHGYNNEFKSMEAIFLAHGPSFKETVIEPFENIEVYLLCDLLHIQ 528
QY 573 PAPNGTHGSLNHLTLWTFRTPTPEVTRPNYPCIMYLOSDFDLCCTDDKVEPKNLD 632
DB 529 PAPNGSHGSLNHLKAPFYQPSHAEELSKSAGCGFTTPLPKDLSNCS - LALQTSQOE 587
QY 633 ELNKLHTGK - - - - -STERHLLYGPVLYLRYR - YDILYHTDFESGYSEIFLMLLTSTYT 687
DB 588 QVNRNLNLSGVEATEKNTLPFGFRVIOKNKHCILYHREIVYSGFGKAMKPMWSST 647
QY 688 VSKQAEVSSVPDLHTSCVRPDVPSFSONCLAYKNQKMSYGFLLPPLYSSTSSPEAKYD 747
DB 648 VPKGDTSSLPPTVDCILRADVRVDPSESQKCSFYLADQNIHGFLLYPPAIKGNESQYD 707

QY 748 AFLVTNMPMPAFKRVNRYFORVLVKKYASRNGVNVISGPIFDYDGLDHTEDKIKQ 807
DB 708 ALITSNLVPMTYKEFKKMDYFHKVLLIKYAIERNGVNVVSGPIFDYNDYGHDFADPEITN 767
QY 808 YVEGSSIVPHTHYYSIITSCDLFTQPADKCDGPLSVSSFILPHRPDNESSCSDESKW 867
DB 768 YVAGTDPVPTHTYFVVLTSCKNKTHTPSCPGWLDVLPFVPHRTNVESCENKAEDLW 827
QY 868 VEELMKMHTARVDRIEHLTSLDFFRKTSSYPEILTLKTLHYLHYSEI 915
DB 828 VEERKAHARVDVELLTGLDFYQEKTPQVSEILQLKYLPTFTETII 875

RESULT 8
P97675 PRELIMINARY; PRT: 875 AA.
AC P97675;
DT 01-MAY-1997 (TREMREL. 03, Created)
DT 01-MAY-1997 (TREMREL. 03, Last sequence update)
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)
DE ALKALINE PHOSPHODIESTERASE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=97250927; PubMed=9096610;
RA Scott L.J., Delautier D., Meerson N.R., Trugnan G., Goding J.W.,
RA Maurice M.;
RT "Biochemical and molecular identification of distinct forms of
RT alkaline phosphodiesterase I expressed on the apical and basolateral
RT plasma membrane surfaces of rat hepatocytes.";
RL Hepatology 25:995-1002(1997).
DR EMBL; U78787; AAB61535.1; -;
DR InterPro; IPR001212; -;
DR InterPro; IPR001604; -;
DR InterPro; IPR002591; -;
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiesterase; 1.
DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 875 AA; 99166 MW; 8FEB9A482173D377 CRC64;

Query Match 41.5%; Score 2081; DB 11; Length 875;
Best Local Similarity 43.5%; Pred. No. 1.7e-161;
Matches 386; Conservative 159; Mismatches 249; Indels 94; Gaps 11;

QY 57 GSKGRCFELQAGPPDCRCDNLCKSVTSCCHDFDELCLKTARGWECTKRCGGEVRNEEN 116
DB 53 GSKKKCFDSHRLGECRCDSGCTDRGCCDWDFETCVKSTQIWTCSNFRCEGTRLEAA 112
QY 117 ACHGSEDCLAGDCCTNYQVVKCGESHVDDDCDEEIKAAECAGFVRPLLIIFSVDGFA 176
DB 113 LSCADDCLORECCCTDYKAVCQGEVPMWTEACASSQEPQCEGDPVVLFSMDGFA 172
QY 177 SYMKKSKVMPNIEKLKSCGTHSPYMPVPTKTPNLYTLATGLYPESHGIVGNSMDP 236
DB 173 EYLQWSTLLPNINKLTKCGLHSHKYMRAVYPTKTPFNHYTIVTGLYPESHGIIIDNNM 232
QY 237 VFDTATHLRGREKFNHWWGQPLWITATKQGVKAGTFW; - - - - -SV 278
DB 233 YLNKNFSLSSVEKSNPAWWSGQPIWLMTAMYGOLKAAASHYWPSCDVAVNGSPFNIRNYSN 292
QY 279 VIPHERILATLRLWLTLPDHERPSVAFYSEQDPFSGHKYGFPGPEESYSGSPFTPAKRP 338
DB 293 SVPTESRIATLLQWLDLPKAERPFYTIYVEEPPDSAGHSGPV; - - - - -SAG 338
QY 339 KRKVAPKRROERPVPAPPKRRRKTHRMHDYAAETRODKMTNPLREIDKIVGOLMDGLKOL 398

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Db 339 -----VICALQLVDDAFGLMEGLKQR 360
QY 399 KLRCVNVIFVGDHGMEDVTCRTEFLSNLTNVDDITLVPGLGRIRSK-----FSNN 452
Db 361 NLHNCVNIIVLADHGMDOQSCDRVEYMTDYFPEI-NFYMYOGPAPRITRNIPODFFTFN 419
QY 453 AKYDPKAIITANCTCKPDQHFQKPYLKOHLPRKRLHYANNRRIEDIHLVRRHWVARKPLD 512
Db 420 S-----EEIVRDLSCRKSDQHFQKPYLTPDLPRKRLHYAKNRIDKVLHMDRWQLAYR---- 471
QY 513 VYKPSGKCFQGDHCFDNKVNMQTVFVGYGTFPKYKVPFENIELYNVMDLLGLK 572
Db 472 --NKGSNC-EGGTHGYNNEFKSMEAIFLAHGPSFKEKTVIEPFENIEVYNLLCDLLHIQ 528
QY 573 PAPNNGTHGSLNHLRTNFRPTMPEVRPNYPGIMYLQSDFDLACTCDDKVEPKNKLD 632
Db 529 PAPNNGSHGSLNHLKAPFYQSHAEELSKSAGCGTTPLPKDSLNCSC-LALQTSQEE 587
QY 633 ELNKLRLHTK-----GSTERHLLYGRPAVLYRTR-YDILYHTDFESGYSEIFLMLLWTSYT 687
Db 588 QVNQRLNLRGEVSATEKTNLPFGPRVQKNKDCHLLYHREYVSGFGKAMKMPMWSYT 647
QY 688 VSKQAEVSSVPHLTSCVRPDRVSPFSQNCLAYKNDKQMSYGFLLPPYLSSEPAAKYD 747
Db 648 VPKPGDTSLLPPTVPDCLRADRVDPSESQKCSFYLDQNDIDHGLFYPAKIGNESQYD 707
QY 748 AFLVTNNVMPYPAFKRVNMYFORVLVKYASERGVNVISGPIFYDYDGLHDTEDKIQ 807
Db 708 ALITSNLVPMYEKFKNMWDYFHKVLLIKYAIERNGVNVSGPIFDYNGHFDAPDEITN 767
QY 808 VEGSSIPVTHYYSITSCDFTQPADKCDGPLSVSFSFILPHRPNESCSNSESDESKW 867
Db 768 YVAGTDPVPVTHYFVLTSCNKNKTHTPDSCPGWLDVLPFVPHRPTNVESCPENKAEDLW 827
QY 868 VEELMKMTARVRDIEHLTSLDFFRKTSRSPYELTLKTYLHTYSEI 915
Db 828 VEERFKAHIAVRDVELLTGLDFYQEKTPQVSEILLQLKTYLPTFETII 875

RESULT 9
P70641 ID P70641 PRELIMINARY; PRT; 876 AA.
AC P70641;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PHOSPHODIESTERASE I.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SMALL INTESTINE, PROXIMAL;
RA Sano K.;
RT "Molecular cloning of phosphodiesterase I cDNA from rat small
RT intestine.";
RL Submitted (May-1994) to the EMBL/GenBank/DDBJ databases.
DR EMBL; D30649; BAA06333.1; -.
DR InterPro; IPR001212; -.
DR InterPro; IPR001604; -.
DR InterPro; IPR002591; -.
DR Pfam; PF01033; Somatomedin_B; 2.
DR Pfam; PF01663; Phosphodiesterase I.
DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART; SM00477; NUC. 1.
SQ SEQUENCE 876 AA; 99328 MW; D2F772C34A0C437A CRC64;

Query Match 41.0%; Score 2057.5; DB 11; Length 876;
Best Local Similarity 43.2%; Pred. No. 1.4e-159;
Matches 384; Conservative 159; Mismatches 251; Indels 95; Gaps 12;
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QY 57 GSKRGRCFELQAEQPPDCRDNLCYSYSCCHDFELCLKTARGWECKTKDRCGEVRNEEN 116
Db 53 GSKRKKCFDSHRGLEGRCDGCTDRGCCWDFEDTKVSTQIWTCSFRCGTRELTA 112
QY 117 ACHSEBCLARGDCCTNYQVCKGESHVWDDCEIEKAAECAPAGFVRPPLIIFSDGGERA 176
Db 113 LCSADCLQKRCDCDQYKAVCOGEVPMVTACASSQBPQCEGFPDQPPVILFSDMGFRA 172
QY 177 SYMKGSKVMPNIEKLSCGTHSPVMPRVYTKTPFPNLYTLATGLYPESHGIVGNSMYDP 236
Db 173 EYLQTSWTLNINKLTCGLHSKYMRAVYTKTPFNHYTIVTGLYPESHGIIDNNMIDV 232
QY 237 VFDAFHLRGREKFNHRMWMGQPLMITATQKGVKAGTEFW-----SV 278
Db 233 YLNKFNLSVSEKSNPAMWSGQIWLTAQYGLKAAASYWPGSDVAVNGSFNIVRYSN 292
QY 279 VIPHERILLITLRLWTLTPDHERPSVIAYSPQDSFGSHKYGFPGEESYSPPTPAKRP 338
Db 293 SVPYESRIATLLQWLDPKAERPSPFTYIYVEEPSAGHKSQPV-----SAG----- 338
QY 339 KRKYAPRRQRQRPVAPPKRRRKIHRNDHYAAETQDKWNTNPLREIDKIVGOLMDGLKQL 398
Db 339 -----VICALQLVDDAFGLMEGLKQR 360
QY 399 KLRCVNVIFVGDHGMEDVTCRTEFLSNLTNVDDITLVPGLGRIRSK-----FSNN 452
Db 361 NLHNCVNIIVLADHGMDOQSCDRVEYMTDYFPEI-NFYMYOGPAPRITRNIPODFFTFN 419
QY 453 AKYDPKAIITANCTCKPDQHFQKPYLKOHLPRKRLHYANNRRIEDIHLVRRHWVARKPLD 512
Db 420 S-----EEIVRDLSCRKSDQHFQKPYLTPDLPRKRLHYAKNRIDKVLHMDRWQLAYR---- 471
QY 513 VYKPSGKCFQGDHCFDNKVNMQTVFVGYGTFPKYKVPFENIELYNVMDLLGLK 572
Db 472 --NKGSNC-EGGTHGYNNEFKSMEAIFLAHGPSFKEKTVIEPFENIEVYNLLCDLLHIQ 528
QY 573 PAPNNGTHGSLNHLRTNFRPTMPEVRPNYPGIMYLQSDFDLACTCDDKVEPKNKLD 632
Db 529 PAPNNGSHGSLNHLKAPFYQSHAEELSKSAGCGTTPLPKDSLNCSC-LALQTSQEE 587
QY 633 ELNKLRLHTK-----GSTERHLLYGRPAVLYRTR-YDILYHTDFESGYSEIFLMLLWTSYT 687
Db 588 QVNQRLNLRGEVSATEKTNLPFGPRVQKNKDCHLLYHREYVSGFGKAMKMPMWSYT 647
QY 688 VSKQAEVSSVPHLTSCVRPDRVSPFSQNCLAYKNDKQMSYGFLLPPYLSSEPAAKYD 747
Db 648 VPKPGDTSLLPPTVPDCLRADRVDPSESQKCSFYLDQNDIDHGLFYPAKIGNESQYD 707
QY 748 AFLVTNNVMPYPAFKRVNMYFORVLVKYASERGVNVISGPIFYDYDGLHDTEDKIQ 807
Db 708 ALITSNLVPMYEKFKNMWDYFHKVLLIKYAIERNGVNVSGPIFDYNGHFDAPDEITN 767
QY 808 VEGSSIPVTHYYSITSCDFTQPADKCDGPLSVSFSFILPHRPNESCSNSESDESK 866
Db 768 YVAGTDPVPVTHYFVLTSCNKNKTHTPDSCPGWLDVLPFVPHRPTNVESCPENKAEDL 827
QY 867 WVEELMKMTARVRDIEHLTSLDFFRKTSRSPYELTLKTYLHTYSEI 915
Db 828 WVEERFKAHIAVRDVELLTGLDFYQEKTPQVSEILLQLKTYLPTFETII 876

RESULT 10
O14638 ID O14638 PRELIMINARY; PRT; 875 AA.
AC O14638;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE BETA (EC 3.1.4.1)
DE (PHOSPHODIESTERASE I BETA).
GN PDNP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

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RL EMBL; AF198100; AAF44374.1; -
DR InterPro; IPR001428; -
DR InterPro; IPR001604; -
DR InterPro; IPR002591; -
DR InterPro; IPR003232; -
DR Pfam; PF01663; Phosphodiester; 1.
DR ProDom; PD000946; -; 1.
DR ProDom; PD004900; -; 1.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 817 AA; 8408 MW; 8404FD00641DA022 CRC64;

Query Match 22.9%; Score 1151; DB 14; Length 817;
Best Local Similarity 32.4%; Pred. No. 1.9e-85;
Matches 263; Conservative 141; Mismatches 276; Indels 132; Gaps 21;

QY 131 CTNYQVCKGSHWDDCEIEKAECAPAGVRPPLIIFSDGFRASYMKKSGKVMNPNI 190
DB 104 CISFGVT-----CPPEFERPPLILIAMNGFRDYLNKWEKIPTIK 144

QY 191 KLRCSHTSPYMRPVYPTKTFNLYLATGLYPESHGIVGNSMYDPVDFATFHLRGEKF 250
DB 145 DLMHGVTAP-MRPVYPTNTFPNLXSVITGLXPISHGIDTNEFIDRGTDIEFTIASEETE 203

QY 251 NHRWGGOPLTATKOGVKAGTFEFW-----SVV-----IPHERILLTLRW 292
DB 204 EWEVGGEPITWITMKNGKSFATFWPGSDKVVPRKRPWYRSYNSKSVPEERINIVLRW 263

QY 293 LTLDPHERPSVYAFYSEQPDFSGHYGPGPESSYSGSPFTPAKRPKRKVPARRQERP 352
DB 264 LKMDTGYRPFYALYLEPGSSGYEG-----290

QY 353 APPKRRRKIHRRMDHYAATRODKWNTNPREDIKVQQLMDGLKQLKLRRCVNVIFVGDH 412
DB 291 -----TDDERVGKALEKVDKATALLMKGLKQLGICCANLILVSDH 331

QY 413 GMEDVTCRTEFLSNVLTNVDITLPGTLGRIRSKFSNNAK-YDPKAIIANLTCKPQD 471
DB 332 GMSNVDPKRVNKLWDYITN-NDVVKPGATPVKIPONLHRLFDYDGIISSTSCVMDQ 390

QY 472 HFKPLKQLHPLKRLHYANNRRIEDHLLVERRHHVARKPLDVKYKPSGKCFQGDHGFON 531
DB 391 PFIYSRSLPKRLHYGSGFTEILGVILEEGWQSDENGNL-KHRSQ-----GPHGSDN 444

QY 532 KVNSMOTVFGVGPFTFKYKTPPENIELYNVMDLLGLKLPAPNNGTHGSLNHLRTNT 591
DB 445 SFQDMTAVFLGYGPAFLDDVRVPIFONIELYNMCEILGINPANNNGTVGSLNHLRNSR 504

QY 592 FRP-----TPPEEVRPNYPGIMYLSQDFDLGCTCD--DKVEPKNKLDELNKRHTKG 642
DB 505 YTHVSSLDIITESECDRHAYVG-----DHKLGCTCKNIDRFSGKNKEDSSR---TRS 555

QY 643 STEERHLYGRPAVLY-RRPYDILYHTDESGYSEIFMLLWTSYTVSKQAESSVSPDHL 701
DB 556 SSYIYNLPFGKPAVLLNRHHHCLINDNVYATYAKVNRPLWTSFSI--DIYTNSTNIYN 613

QY 702 TSCVRPDVRSFSQNCIAYKNDKOMSYGFLFPYLSSSPEAKYDAFLVNNMVPMPAF 761
DB 614 KTCYLQDMRVM-YYPEPCRYSTQKQDVTGYLYP-----ARATDFQSLLTETNTPMYRNF 667

QY 762 KRVNRYFORVLVKKYASERNGVNVISGPIFDYDGLHTEDEKIKO---YVEGSSIPVPT 818
DB 668 KKIWEVFMSSILIEYVQKHVVNVMGVPVFDNSNGIRDSNGLISMSGYY--NNKYVIPS 725

QY 819 HYSIITSCLDFTQPADKCDGPLSVSSFTLPHRPD-NEESCSNSEDSE-KWVEELMKMHT 876
DB 726 DYFVLTTCOKDSSLNDCYSNIKTESFVVPNSDFTYNEESCRENITTSVYVKRIFSLHR 785

QY 877 ARVRDIEHTLSLDFRKTSSYPEILITLTKYL 908
DB 786 VRIKDIEVTSNFSYRNKYKTSNVAYLKTYM 817
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RESULT 15
Q9SU82 PRELIMINARY; PRT; 457 AA.
AC Q9SU82;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE NUCLEOTIDE PYROPHOSPHATASE-LIKE PROTEIN (EC 3.6.1.9).
GN T16L4.200 OR AT4G29690.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID:3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Rose M., Hempel S., Entian K.-D., Bancroft I., Mewes H.W.,
RA Mayer K.F.X., Lemcke K., Schueller C.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL079344; CAB45329.1; -
DR EMBL; AL161575; CAB79727.1; -
DR InterPro; IPR002591; -
DR Pfam; PF01663; Phosphodiester; 1.
KW Hydrolase.
SQ SEQUENCE 457 AA; 51261 MW; 3B95B6C0AE1B1215 CRC64;
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Query Match 12.9%; Score 646.5; DB 10; Length 457;
Best Local Similarity 32.0%; Pred. No. 1.5e-44;
Matches 151; Conservative 78; Mismatches 136; Indels 107; Gaps 12;

QY 146 DDCEEIKAAECAPAGVRPPLIIFSDGFRASYMKKSGKVMNPNIKLRCSCTHSPY-MRP 204
DB 37 DSPSSYVRRPQPKLKNKPVVLLISCDFRGFGYFKTE--TPNIDLLISRGTEAKTGLIP 94

QY 205 VYPTKTPNLYLATGLYPESHGIVGNSMYDPVDFATFHLRGEKFNHRWGGOPLTWTA 264
DB 95 VFPTMTFPNHYSIATGLYPASHGIIMNKFTDPVSGELFN-----RNLNPKWLGLPLMWTA 150

QY 265 TKQGVKAGTFFW-----SVVIPHERRILTLRWLTLPQHERPSV 303
DB 151 VNQGLMAATYFWPCADYHKGSNCKPGCKACAPYNSVPLEERVDTILNYFDLPEREIPDF 210

QY 304 YAFYSEOPDPSGHYKYPGPEESSYSGSPFTPAKRPKRKVPARRQERPVPAPKRRRIKH 363
DB 211 MALYFDEPDIQGEHYGPDPP-----230

QY 364 RMDHYAETRODKWNTNPREDIKVQQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCRTE 423
DB 231 -----RVTEAVSKYDKRMIGRIIMGLEKRRKVFSDHVILLGDHGMV--TNCDDKV 277

QY 424 FLSNLTNVDITLVPG-----TLGR-IRSKFSNNAKYDPKAIIANLTCKK 468
DB 278 I---YIIDLADWIKIPADWIODYSPVLAAMPNRPWKDKVKNPCQKNAELVRKNEALSSSKV 334

QY 469 PQDHF-KPYLKQHLPLKRLHYANNRRIEDHLLVERRHHVARKPLDVKYKPSGKCFQGDH 527
DB 335 ANGEFLQYLKENLPQRLHYSDSSRIPIIGMVGEGLMVKQNRITYVQ-----EC--SGTH 387

QY 528 GFDNKNVSMQTVFVGYPGTFKTKYKPPFPFENIELYNVMDLLGLKLPAPNNGT 579
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Db 388 GYDNFFSMRSIFVGYGPRRRGKVPSEFNQVYNVAEILGLRPAPNGS 439

Search completed: July 19, 2001, 14:46:48
Job time: 171 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2001, 14:45:00 ; Search time 34.65 Seconds
(without alignments)
22.745 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213
Perfect score: 76
Sequence: 1 YMRPVPTKTFN 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601.*
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21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	13	AA1992	Autotaxin phosphod
2	76	100.0	788	AA198579	Autotaxin derived
3	76	100.0	829	AA198578	Autotaxin derived
4	76	100.0	858	AA191985	Rat autotaxin prot
5	76	100.0	858	AA191985	Rat autotaxin vari
6	76	100.0	858	AA191986	Rat autotaxin vari
7	76	100.0	858	AA191987	Rat autotaxin vari
8	76	100.0	858	AA191988	Rat autotaxin vari
9	76	100.0	858	AA191989	Rat autotaxin vari
10	76	100.0	859	AA191991	Human autotaxin pr
11	76	100.0	863	AA191988	Human teratocarcin

12	76	100.0	915	17	AA198596	A2038 autotaxin pr
13	76	100.0	915	22	AA191987	Human melanoma aut
14	76	100.0	979	17	AA198580	Autotaxin derived
15	71	93.4	849	17	AA198595	N-tera 2D1 autotax
16	70	92.1	885	22	AA191989	Rat brain autotaxi
17	69	90.8	873	21	AA1983620	Human PC-1 polyep
18	69	90.8	873	21	AA1983621	Variant human PC-1
19	69	90.8	925	16	AA1979148	Human insulin rece
20	69	90.8	925	20	AA1939355	Insulin receptor t
21	69	90.8	925	21	AA1900195	Breast cancer prot
22	49	64.5	400	21	AA1929475	Arabidopsis thalia
23	49	64.5	457	21	AA1931321	Arabidopsis thalia
24	49	64.5	461	21	AA1929474	Arabidopsis thalia
25	49	64.5	465	21	AA1929473	Arabidopsis thalia
26	43	56.6	173	20	AA197084	Renal cancer assoc
27	43	56.6	263	18	AA1940374	Human breast cance
28	43	56.6	263	18	AA1901573	Protein encoded by
29	43	56.6	263	21	AA1984037	Amino acid sequenc
30	43	56.6	562	21	AA1953329	Human colon cancer
31	43	56.6	579	18	AA1940378	Human breast cance
32	43	56.6	579	21	AA1984041	Amino acid sequenc
33	42	55.3	411	20	AA1934445	Porphyromonas ging
34	42	55.3	428	20	AA1934324	Porphyromonas ging
35	42	55.3	528	22	AA1979259	Corynebacterium gl
36	42	55.3	530	22	AA1979258	Corynebacterium gl
37	41	53.9	109	19	AA1952839	Secreted protein e
38	41	53.9	453	20	AA1917529	Human secreted pro
39	41	53.9	453	20	AA1902378	Polypeptide ident
40	41	53.9	453	22	AA1990545	Human secreted pro
41	40	52.6	199	21	AA1944375	Arabidopsis thalia
42	40	52.6	199	21	AA1953821	Arabidopsis thalia
43	40	52.6	199	22	AA1968971	Sheep mitosis arre
44	40	52.6	199	22	AA1968972	Human mitosis arre
45	40	52.6	205	18	AA1913020	Human MAD2 protein

ALIGNMENTS

RESULT 1
AA191992
ID AA191992 standard; peptide; 13 AA.

XX AA191992;
AC AA191992;
DT 28-MAR-2001 (first entry)
DE Autotaxin phosphodiesterase catalytic site.

XX Autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity;
KW phosphodiesterase catalytic site.

XX Unidentified.
OS XX
PN WO200068386-A1.
PD 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US12402.
XX 07-MAY-1999; 99US-0306979.
PA (ZYMO) ZYMOGENETICS INC.
PI Kelly JD;
DR WPI; 2001-007397/01.

PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 XX Disclosure; Page 3; 126pp; English.
 XX
 CC The present sequence is autotaxin phosphodiesterase catalytic
 CC site. Phosphorylation of threonine residue at position 10 of this
 CC sequence is required for autotaxin to undergo autophosphorylation
 CC and exhibit phosphodiesterase and motility-stimulating activities.
 CC Autotaxin is a glycoprotein cytokine which increases
 CC insulin signalling in adipose tissue by producing substrate for
 CC adenosine receptors, resulting in inhibition of lipolysis, and
 CC decreased hepatic gluconeogenesis and serum glucose levels, and
 CC increased insulin sensitivity. It also inhibits differentiation
 CC of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-
 CC triphosphatase (ATPase) and ATP pyrophosphatase activities.
 CC Autotaxin and its analogues are used to stimulate glucose uptake
 CC by cells, particularly to reduce serum glucose levels for
 CC treatment of non-insulin dependent diabetes (NIDDM) in humans,
 CC or generally any condition associated with elevated serum levels
 CC of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
 CC Transgenic animals that overexpress autotaxin are models for
 CC human metabolic diseases.
 XX
 XX Sequence 13 AA;

Query Match 100.0%; Score 76; DB 22; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 |||||
 Db 1 ymrpyptktfnp 13

RESULT 2

AAR86579
 ID AAR86579 standard; Protein; 788 AA.
 AC AAR86579;
 XX
 XX 28-JUN-1996 (first entry)
 XX
 DE Autotaxin derived from teratocarcinoma N-tera 2D1 cells.
 XX
 KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
 KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9532221-A2.
 XX
 PD 30-NOV-1995.
 XX
 XX 24-MAY-1995; 95WO-US06613.
 XX
 XX 28-NOV-1994; 94US-0346455.
 PR 25-MAY-1994; 94US-0249182.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Krutzech J, Liotta L, Murata J, Schiffmann E, Stracke M;
 XX WPI; 1996-020533/02.
 DR N-PSDB; AAT06613.
 XX
 XX Autotaxin motility stimulating protein, and DNA encoding it - used
 PT in cancer diagnosis and therapy
 XX
 XX Claim 4; Page 62-65; 112pp; English.
 PS
 XX AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is

CC an autocrine motility stimulating protein which is present in cancer
 CC cells. ATX stimulates both random and directed migration of melanoma
 CC cells. The tumorous form of ATX is a secreted protein, while the
 CC transmembrane bound form is not present in tumour cells. The cDNA
 CC encoding this sequence can be used in a vector, to transform cells.
 CC recombinant cells can then be used to produce the peptide sequences.
 CC Antibodies specific for these sequences can be produced, and can be used
 CC in cancer diagnosis and therapy. Different sites of localisation of the
 CC protein are utilised for diagnosis and prognosis of the stages of tumour
 CC progression. The sequences can be used in treatment methods to
 CC advantageously block the activity of the secreted form of ATX, while
 CC having little effect on the membrane form of ATX.

XX Sequence 788 AA;

Query Match 100.0%; Score 76; DB 17; Length 788;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 |||||
 Db 126 ymrpyptktfnp 138

RESULT 3

AAR86578
 ID AAR86578 standard; Protein; 829 AA.
 XX
 AC AAR86578;
 XX
 XX 28-JUN-1996 (first entry)
 XX
 DE Autotaxin derived from melanoma cell line A2058.
 XX
 KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
 KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9532221-A2.
 XX
 PD 30-NOV-1995.
 XX
 XX 24-MAY-1995; 95WO-US06613.
 XX
 XX 28-NOV-1994; 94US-0346455.
 PR 25-MAY-1994; 94US-0249182.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Krutzech J, Liotta L, Murata J, Schiffmann E, Stracke M;
 XX WPI; 1996-020533/02.
 DR N-PSDB; TO6612.
 XX
 XX Autotaxin motility stimulating protein, and DNA encoding it - used
 PT in cancer diagnosis and therapy
 XX
 XX Claim 4; Page 57-60; 112pp; English.
 XX
 XX AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is
 CC an autocrine motility stimulating protein which is present in cancer
 CC cells. ATX stimulates both random and directed migration of melanoma
 CC cells. The tumorous form of ATX is a secreted protein, while the
 CC transmembrane bound form is not present in tumour cells. The cDNA
 CC encoding this sequence can be used in a vector, to transform cells.
 CC recombinant cells can then be used to produce the peptide sequences.
 CC Antibodies specific for these sequences can be produced, and can be used
 CC in cancer diagnosis and therapy. Different sites of localisation of the
 CC protein are utilised for diagnosis and prognosis of the stages of tumour
 CC progression. The sequences can be used in treatment methods to
 CC advantageously block the activity of the secreted form of ATX, while
 CC having little effect on the membrane form of ATX.

CC having little effect on the membrane form of AXT.

XX Sequence 829 AA;

SQ Query Match 100.0%; Score 76; DB 17; Length 829;

Best Local Similarity 100.0%; Pred. No. 0.00013;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13

Db 115 ymrpvptktfnp 127

RESULT 4

RAY71986

ID AAY71986 standard; Protein; 858 AA.

XX AC AAY71986;

DT 28-MAR-2001 (first entry)

DE Rat autotaxin protein.

XX Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine-5'-triphosphatase activity.

XX OS Rattus sp.

XX Key Location/Qualifiers

FT Domain 5..15

FT Binding-site /note= "Putative transmembrane domain"

FT Region 122..124

FT Region 143..158

FT Region /label= Epitope

FT Region /note= "This region is specifically claimed in claim 10"

FT Region /label= Epitope

FT Region /note= "This region is specifically claimed in claim 10;

FT Region This region is absent in rat brain autotaxin designated

FT Region as PD-1alpha sequence (AAY71989)"

FT Active-site 196..208

FT Region /note= "Autotaxin phosphodiesterase catalytic site"

FT Region 585..595

FT Region /label= Epitope

FT Region /note= "This region is specifically claimed in claim 10"

FT WO200068386-A1.

PN 16-NOV-2000.

PD 05-MAY-2000; 2000WO-US12402.

XX 07-MAY-1999; 99US-0306979.

XX (ZYMO) ZYMOGENETICS INC.

XX Kelly JD;

XX WPI; 2001-007397/01.

DR N-PSDB; AAD02131.

XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and

XX obesity, stimulate glucose uptake by cells and inhibit lipolysis -

XX Claim 1; Page 101-104; 126pp; English.

XX The present sequence is rat autotaxin protein. Autotaxin is a

CC

CC glycoprotein cytokine which increases insulin
 CC signalling in adipose tissue by producing substrate for adenosine
 CC receptors, resulting in inhibition of lipolysis, decreased hepatic
 CC gluconeogenesis and serum glucose levels, and increased insulin
 CC sensitivity. It also inhibits differentiation of adipocytes.
 CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
 CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
 CC analogues are used to stimulate glucose uptake by cells, particularly
 CC to reduce serum glucose levels for treatment of non-insulin dependent
 CC diabetes (NIDDM) in humans, or generally any condition associated
 CC with elevated serum levels of glucose, lipid or free fatty acid
 CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
 CC autotaxin are models for human metabolic diseases.

XX Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;

Best Local Similarity 100.0%; Pred. No. 0.00014;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13

Db 196 ymrpvptktfnp 208

RESULT 5

AAY71995

ID AAY71995 standard; Protein; 858 AA.

XX AC AAY71995;

DT 28-MAR-2001 (first entry)

DE Rat autotaxin variant (A93V).

XX Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine-5'-triphosphatase activity; mutant; variant.

XX OS Rattus sp.

XX Synthetic.

XX Key . Location/Qualifiers

FT Misc-difference 93

FT /note= "Wild type Ala substituted by Val"

XX WO200068386-A1.

PN 16-NOV-2000.

PD 05-MAY-2000; 2000WO-US12402.

XX 07-MAY-1999; 99US-0306979.

XX (ZYMO) ZYMOGENETICS INC.

XX Kelly JD;

XX WPI; 2001-007397/01.

XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and

XX obesity, stimulate glucose uptake by cells and inhibit lipolysis -

XX Disclosure; Page -; 126pp; English.

XX The present sequence is variant (A93V) of rat autotaxin protein.

XX Autotaxin is a glycoprotein cytokine which increases insulin

XX signalling in adipose tissue by producing substrate for adenosine

XX receptors, resulting in inhibition of lipolysis, decreased hepatic

CC

CC gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes.
 CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP pyrophosphatase activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases.
 CC Note: The present sequence is not shown in the specification but is derived from rat autotaxin protein sequence found in page 101-104 of sequence listing (AAY71986).
 CC
 XX
 SQ Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 |||||
 Db 196 ymrpvypkttfn 208

RESULT 6
 AAY71996
 ID AAY71996 standard; Protein; 858 AA.
 XX
 AC AAY71996;
 XX
 DT 28-MAR-2001 (first entry)
 XX
 DE Rat autotaxin variant (A194V).
 XX

KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose; KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; KW type I phosphodiesterase activity; ATP pyrophosphatase activity; KW ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.
 XX
 OS Rattus sp.
 OS Synthetic.

XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 194 /note= "Wild type Ala substituted by Val"
 FT
 XX WO200068386-A1.
 XX
 PD 16-NOV-2000.
 XX
 XX 05-MAY-2000; 2000WO-US12402.
 XX
 XX 07-MAY-1999; 99US-0306979.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Kelly JD;
 XX
 XX WPI; 2001-007397/01.
 XX

XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 XX
 XX Disclosure; Page -: 126pp; English.
 XX
 XX The present sequence is variant (A194V) of rat autotaxin protein.
 CC Autotaxin is a glycoprotein cytokine which increases insulin
 CC signalling in adipose tissue by producing substrate for adenosine
 CC receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes.
 CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP pyrophosphatase activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases.
 CC Note: The present sequence is not shown in the specification but is derived from rat autotaxin protein sequence found in page 101-104 of sequence listing (AAY71986).
 CC
 XX
 SQ Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 |||||
 Db 196 ymrpvypkttfn 208

RESULT 7
 AAY71997
 ID AAY71997 standard; Protein; 858 AA.
 XX
 AC AAY71997;
 XX
 DT 28-MAR-2001 (first entry)
 XX
 DE Rat autotaxin variant (S236T).
 XX

KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose; KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; KW type I phosphodiesterase activity; ATP pyrophosphatase activity; KW ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.
 XX
 OS Rattus sp.
 OS Synthetic.

XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 236 /note= "Wild type Ser substituted by Thr"
 FT
 XX WO200068386-A1.
 XX
 PD 16-NOV-2000.
 XX
 XX 05-MAY-2000; 2000WO-US12402.
 XX
 XX 07-MAY-1999; 99US-0306979.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Kelly JD;
 XX
 XX WPI; 2001-007397/01.
 XX

XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 XX
 XX Disclosure; Page -: 126pp; English.
 XX
 XX The present sequence is variant (S236T) of rat autotaxin protein.
 CC Autotaxin is a glycoprotein cytokine which increases insulin
 CC signalling in adipose tissue by producing substrate for adenosine
 CC receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin
 CC sensitivity. It also inhibits differentiation of adipocytes.
 CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
 CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
 CC analogues are used to stimulate glucose uptake by cells, particularly
 CC to reduce serum glucose levels for treatment of non-insulin dependent
 CC diabetes (NIDDM) in humans, or generally any condition associated
 CC with elevated serum levels of glucose, lipid or free fatty acid
 CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
 CC autotaxin are models for human metabolic diseases.
 CC Note: The present sequence is not shown in the specification
 CC but is derived from rat autotaxin protein sequence found in
 CC page 101-104 of sequence listing (AA71986).
 XX
 SQ Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 |||||
 Db 196 ymrpvptktfnp 208

RESULT 8
 AAY71998
 ID AAY71998 standard; Protein: 858 AA.
 XX
 AC AAY71998;
 XX
 DT 28-MAR-2001 (first entry)
 XX
 DE Rat autotaxin variant (R265K).
 XX
 KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.
 XX
 OS Rattus sp.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 265 /note= "Wild type Arg substituted by Lys"
 FT
 XX
 PN WO200068386-A1.
 XX
 PD 16-NOV-2000.
 XX
 PF 05-MAY-2000; 2000WO-US12402.
 XX
 PR 07-MAY-1999; 99US-0306979.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Kelly JD;
 XX
 DR WPI; 2001-007397/01.
 XX
 PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 XX
 PS Disclosure; Page -: 126pp; English.
 XX
 CC The present sequence is variant (R265K) of rat autotaxin protein.
 CC Autotaxin is a glycoprotein cytokine which increases insulin
 CC signalling in adipose tissue by producing substrate for adenosine
 CC receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin
 CC sensitivity. It also inhibits differentiation of adipocytes.
 CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
 CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
 CC analogues are used to stimulate glucose uptake by cells, particularly
 CC to reduce serum glucose levels for treatment of non-insulin dependent
 CC diabetes (NIDDM) in humans, or generally any condition associated
 CC with elevated serum levels of glucose, lipid or free fatty acid
 CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
 CC autotaxin are models for human metabolic diseases.
 CC Note: The present sequence is not shown in the specification
 CC but is derived from rat autotaxin protein sequence found in
 CC page 101-104 of sequence listing (AA71986).
 XX
 SQ Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 |||||
 Db 196 ymrpvptktfnp 208

RESULT 9
 AAY71999
 ID AAY71999 standard; Protein: 858 AA.
 XX
 AC AAY71999;
 XX
 DT 28-MAR-2001 (first entry)
 XX
 DE Rat autotaxin variant (S289T).
 XX
 KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.
 XX
 OS Rattus sp.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 289 /note= "Wild type Ser substituted by Thr"
 FT
 XX
 PN WO200068386-A1.
 XX
 PD 16-NOV-2000.
 XX
 PF 05-MAY-2000; 2000WO-US12402.
 XX
 PR 07-MAY-1999; 99US-0306979.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Kelly JD;
 XX
 DR WPI; 2001-007397/01.
 XX
 PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 XX
 PS Disclosure; Page -: 126pp; English.
 XX
 CC The present sequence is variant (S289T) of rat autotaxin protein.
 CC Autotaxin is a glycoprotein cytokine which increases insulin
 CC signalling in adipose tissue by producing substrate for adenosine
 CC receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin
CC sensitivity. It also inhibits differentiation of adipocytes.
CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
CC analogues are used to stimulate glucose uptake by cells, particularly
CC to reduce serum glucose levels for treatment of non-insulin dependent
CC diabetes (NIDDM) in humans, or generally any condition associated
CC with elevated serum levels of glucose, lipid or free fatty acid
CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
CC autotaxin are models for human metabolic diseases.
CC Note: The present sequence is not shown in the specification
CC but is derived from rat autotaxin protein sequence found in
CC page 101-104 of sequence listing (AA71986).
XX
SQ Sequence 858 AA;

Query Match 100.0%; Score 76; DB 22; Length 858;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
| | | | | | | | | | | | | | |
Db 196 ymrpvpyptktpn 208

RESULT 10
AA71991
ID AAY71991 standard; Protein: 859 AA.
XX
AC AAY71991;
XX
DT 28-MAR-2001 (first entry)
XX
DE Human autotaxin protein.
XX
KW Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 8..26 /note= "Putative transmembrane domain"
FT Cleavage-site 44..45
FT Binding-site 123..125 /label= RGD_binding_domain
FT Active-site 197..209 /note= "Putative phosphodiesterase active site"
FT
XX
PN WO200068386-A1.
XX
XX 16-NOV-2000.
XX
XX 05-MAY-2000; 2000WO-US12402.
XX
XX 07-MAY-1999; 99US-0306979.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Kelly JD;
XX
XX WPI; 2001-007397/01.
XX N-PSDB; AAD02133.
XX
XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and
XX obesity, stimulate glucose uptake by cells and inhibit lipolysis -
XX
XX Claim 27; Page 119-121; 126pp; English.

XX
CC The present sequence is human autotaxin protein.
CC Autotaxin is a glycoprotein cytokine which increases
CC insulin signalling in adipose tissue by producing substrate for
CC adenosine receptors, resulting in inhibition of lipolysis, and
CC decreased hepatic gluconeogenesis and serum glucose levels, and
CC increased insulin sensitivity. It also inhibits differentiation
CC of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-
CC triphosphatase (ATPase) and ATP pyrophosphatase activities.
CC Autotaxin and its analogues are used to stimulate glucose uptake
CC by cells, particularly to reduce serum glucose levels for
CC treatment of non-insulin dependent diabetes (NIDDM) in humans,
CC or generally any condition associated with elevated serum levels
CC of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
CC Transgenic animals that overexpress autotaxin are models for
CC human metabolic diseases.
XX
SQ Sequence 859 AA;

Query Match 100.0%; Score 76; DB 22; Length 859;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
| | | | | | | | | | | | | | |
Db 197 ymrpvpyptktpn 209

RESULT 11
AA71988
ID AAY71988 standard; Protein: 863 AA.
XX
AC AAY71988;
XX
DT 28-MAR-2001 (first entry)
XX
DE Human teratocarcinoma autotaxin.
XX
KW Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity; teratocarcinoma.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Binding-site 127..129 /label= RGD_binding_domain
FT Active-site 201..213 /note= "Autotaxin phosphodiesterase catalytic site"
FT
XX
PN WO200068386-A1.
XX
XX 16-NOV-2000.
XX
XX 05-MAY-2000; 2000WO-US12402.
XX
XX 07-MAY-1999; 99US-0306979.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Kelly JD;
XX
XX WPI; 2001-007397/01.
XX
XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and
XX obesity, stimulate glucose uptake by cells and inhibit lipolysis -
XX
XX Claim 27; Page 108-110; 126pp; English.

CC The present sequence is autotaxin isolated from human
 CC teratocarcinoma cells. Autotaxin is a glycoprotein cytokine which
 CC increases insulin signalling in adipose tissue by producing substrate
 CC for adenosine receptors, resulting in inhibition of lipolysis.
 CC decreased hepatic gluconeogenesis and serum glucose levels, and
 CC increased insulin sensitivity. It also inhibits differentiation
 CC of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-
 CC triphosphatase (ATPase) and ATP pyrophosphatase activities.
 CC Autotaxin and its analogues are used to stimulate glucose uptake
 CC by cells, particularly to reduce serum glucose levels for
 CC treatment of non-insulin dependent diabetes (NIDDM) in humans,
 CC or generally any condition associated with elevated serum levels
 CC of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
 CC Transgenic animals that overexpress autotaxin are models for
 CC human metabolic diseases.

XX Sequence 863 AA;

Query Match 100.0%; Score 76; DB 22; Length 863;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
 |||||
 Db 201 ymrpvyptktpn 213

RESULT 12

AAR86596
 ID AAR86596 standard; Protein; 915 AA.

AC AAR86596;

DT 01-JUL-1996 (first entry)

DE A2058 autotaxin protein.

KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
 KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.

OS Homo sapiens.

PN W09532221-A2.

PD 30-NOV-1995.

PF 24-MAY-1995; 95WO-US06613.

PR 28-NOV-1994; 94US-0346455.

PR 25-MAY-1994; 94US-0249182.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;

XX WPI; 1996-020533/02.

XX Autotaxin motility stimulating protein, and DNA encoding it - used
 in cancer diagnosis and therapy

PS Claim 4; Page 91-94; 112pp; English.

XX AAR86559-R86596 represent autotaxin (ATX) and fragments of it. This
 CC sequence represents the full length protein sequence of the A2058
 CC melanoma cell line ATX protein. ATX is an autocrine motility
 CC stimulating protein which is present in cancer cells. ATX stimulates
 CC both random and directed migration of melanoma cells. The tumorous form
 CC of ATX is a secreted protein, while the transmembrane bound form is not
 CC present in tumour cells. The cDNA encoding this sequence can be used in
 CC a vector, to transform cells. The recombinant cells can then be used to
 CC produce the peptide sequences. Antibodies specific for these sequences
 CC can be produced, and can be used in cancer diagnosis and therapy.

CC Different sites of localisation of the protein are utilised for diagnosis
 CC and prognosis of the stages of tumour progression. The sequences can be
 CC used in treatment methods to advantageously block the activity of the
 CC secreted form of ATX, while having little effect on the membrane form of
 CC ATX.

XX Sequence 915 AA;

Query Match 100.0%; Score 76; DB 17; Length 915;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
 |||||
 Db 201 ymrpvyptktpn 213

RESULT 13

AAY71987
 ID AAY71987 standard; Protein; 915 AA.

AC AAY71987;

DT 28-MAR-2001 (first entry)

DE Human melanoma autotaxin.

KW Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine-5'-triphosphatase activity; melanoma.

OS Homo sapiens.

Key Location/Qualifiers

FT Binding-site 127..129

FT /label= RGD_binding_domain

FT Active-site 201..213

FT /note= "Autotaxin phosphodiesterase catalytic site"

PN W0200068386-A1.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US12402.

XX 07-MAY-1999; 99US-0306979.

XX (ZYMO) ZYMOGENETICS INC.

XX Kelly JD;

XX WPI; 2001-007397/01.

XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -

XX Claim 27; Page 105-108; 126pp; English.

XX The present sequence is autotaxin isolated from human melanoma
 CC cells. Autotaxin is a glycoprotein cytokine which increases
 CC insulin signalling in adipose tissue by producing substrate for
 CC adenosine receptors, resulting in inhibition of lipolysis, and
 CC decreased hepatic gluconeogenesis and serum glucose levels, and
 CC increased insulin sensitivity. It also inhibits differentiation
 CC of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-
 CC triphosphatase (ATPase) and ATP pyrophosphatase activities.
 CC Autotaxin and its analogues are used to stimulate glucose uptake
 CC by cells, particularly to reduce serum glucose levels for
 CC treatment of non-insulin dependent diabetes (NIDDM) in humans,

CC or generally any condition associated with elevated serum levels
CC of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
CC Transgenic animals that overexpress autotaxin are models for
CC human metabolic diseases.
XX Sequence 915 AA;
SQ
Query Match 100.0%; Score 76; DB 22; Length 915;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YMRPVYPTKTFPN 13
Db 201 ymrpvpytktfpn 213
|||||
RESULT 14
AAR86580
ID AAR86580 standard; Protein; 979 AA.
XX AC
XX AAR86580;
XX 28-JUN-1996 (first entry)
XX Autotaxin derived from human liver cells.
XX
XX Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
XX melanoma cell; tumour; antibody; cancer diagnosis; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Misc-difference 864 /note= "unspecified amino acid"
FT Misc-difference 889 /note= "unspecified amino acid"
FT Misc-difference 905 /note= "unspecified amino acid"
FT Misc-difference 911 /note= "unspecified amino acid"
FT Misc-difference 927 /note= "unspecified amino acid"
FT Misc-difference 937 /note= "unspecified amino acid"
FT Misc-difference 944 /note= "unspecified amino acid"
FT Misc-difference 950 /note= "unspecified amino acid"
FT Misc-difference 954 /note= "unspecified amino acid"
FT Misc-difference 967 /note= "unspecified amino acid"
FT Misc-difference 975 /note= "unspecified amino acid"
XX W09532221-A2.
XX
XX 30-NOV-1995.
XX
XX 24-MAY-1995; 95WO-US06613.
XX
XX 28-NOV-1994; 94US-0346455.
XX 25-MAY-1994; 94US-0249182.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;
XX WPI; 1996-020533/02.
XX Autotaxin motility stimulating protein, and DNA encoding it - used
PT in cancer diagnosis and therapy

XX Claim 4; Page 67-70; 112pp; English.
XX AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is
CC an autocrine motility stimulating protein which is present in cancer
CC cells. ATX stimulates both random and directed migration of melanoma
CC cells. The tumorous form of ATX is a secreted protein, while the
CC transmembrane bound form is not present in tumour cells. The cDNA
CC encoding this sequence can then be used in a vector, to transform cells.
CC Recombinant cells can then be used to produce the peptide sequences.
CC Antibodies specific for these sequences can be produced, and can be used
CC in cancer diagnosis and therapy. Different sites of localisation of the
CC protein are utilised for diagnosis and prognosis of the stages of tumour
CC progression. The sequences can be used in treatment methods to
CC advantageously block the activity of the secreted form of AXT, while
XX having little effect on the membrane form of AXT.
XX Sequence 979 AA;
SQ
Query Match 100.0%; Score 76; DB 17; Length 979;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YMRPVYPTKTFPN 13
Db 201 ymrpvpytktfpn 213
|||||
RESULT 15
AAR86595
ID AAR86595 standard; Protein; 849 AA.
XX AC
XX AAR86595;
XX 01-JUL-1996 (first entry)
XX N-tera 2D1 autotaxin protein.
XX
XX Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
XX melanoma cell; tumour; antibody; cancer diagnosis; therapy.
XX Homo sapiens.
XX OS
XX W09532221-A2.
XX
XX 30-NOV-1995.
XX
XX 24-MAY-1995; 95WO-US06613.
XX
XX 28-NOV-1994; 94US-0346455.
XX 25-MAY-1994; 94US-0249182.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;
XX WPI; 1996-020533/02.
XX Autotaxin motility stimulating protein, and DNA encoding it - used
PT in cancer diagnosis and therapy
XX
XX Claim 4; Page 86-89; 112pp; English.
XX AAR86559-R86596 represent autotaxin (ATX) and fragments of it. This
CC sequence represents the full length protein sequence of the
CC teratocarcinoma N-tera 2D1 ATX protein. ATX is an autocrine motility
CC stimulating protein which is present in cancer cells. ATX stimulates
CC both random and directed migration of melanoma cells. The tumorous
CC form of ATX is a secreted protein, while the transmembrane bound form is
CC not present in tumour cells. The cDNA encoding this sequence can be used
CC in a vector, to transform cells. The recombinant cells can then be used
CC to produce the peptide sequences. Antibodies specific for these

CC sequences can be produced, and can be used in cancer diagnosis and
CC therapy. Different sites of localisation of the protein are utilised for
CC diagnosis and prognosis of the stages of tumour progression. The
CC sequences can be used in treatment methods to advantageously block the
CC activity of the secreted form of AXI, while having little effect on the
CC membrane form of AXI.

XX

SQ Sequence 849 AA;

Query Match 93.48; Score 71; DB 17; Length 849;
Best Local Similarity 92.38; Pred. No. 0.00091;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13

Db 201 hmrpvptktfnp 213
:|||||

Search completed: July 19, 2001, 14:45:00
Job time: 208 sec

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OM protein - protein search, using sw model

Run on: July 23, 2001, 13:16:07 ; Search time 20.3 seconds
(without alignments)
12.901 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213
Perfect score: 76
Sequence: 1 YMRPVYPTKTFPN 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	788	1	US-08-346-455B-36
2	76	100.0	788	3	US-08-977-221-36
3	76	100.0	788	5	PCT-US95-06613-36
4	76	100.0	829	1	US-08-346-455B-34
5	76	100.0	829	3	US-08-977-221-34
6	76	100.0	829	5	PCT-US95-06613-34
7	76	100.0	915	1	US-08-346-455B-69
8	76	100.0	915	3	US-08-977-221-69
9	76	100.0	915	5	PCT-US95-06613-69
10	76	100.0	979	1	US-08-346-455B-38
11	76	100.0	979	3	US-08-977-221-38
12	76	100.0	979	5	PCT-US95-06613-38
13	71	93.4	861	1	US-08-346-455B-67
14	71	93.4	861	3	US-08-977-221-67
15	71	93.4	861	5	PCT-US95-06613-67
16	69	90.8	873	3	US-09-187-331-6
17	69	90.8	925	2	US-08-392-946-1
18	69	90.8	925	2	US-08-504-169-1
19	69	90.8	925	5	PCT-US94-14893-1
20	40	52.6	203	2	US-08-684-024-8
21	40	52.6	203	2	US-09-145-868-8
22	40	52.6	205	2	US-08-684-024-1
23	40	52.6	205	2	US-08-684-024-6
24	40	52.6	205	2	US-08-684-024-7
25	40	52.6	205	3	US-09-145-868-1
26	40	52.6	205	3	US-09-145-868-6
27	40	52.6	205	3	US-09-145-868-7

Sequence 2, Appli
Sequence 6, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 120, App
Sequence 120, App
Sequence 120, App
Sequence 8, Appli
Sequence 8, Appli
Sequence 5, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 10, Appli
Sequence 6, Appli
Sequence 18, Appli
Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-346-455B-36
; Sequence 36, Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,455B
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 788
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein

```

;
; HYPOTHETICAL: NO
; ORIGINAL SOURCE: Human
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: teratocarcinoma
; CELL LINE: N-tera 2D1
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: N-tera 2D1 putative
; OTHER INFORMATION: ATX protein sequence
;
US-08-346-455B-36

Query Match 100.0%; Score 76; DB 1; Length 788;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
Db 126 YMRPVYPTKTFPN 138

RESULT 2
US-08-977-221-36
; Sequence 36, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 36:

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 788
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: teratocarcinoma
; CELL LINE: N-tera 2D1
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: N-tera 2D1 putative
; OTHER INFORMATION: ATX protein sequence
;
US-08-977-221-36

Query Match 100.0%; Score 76; DB 3; Length 788;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
Db 126 YMRPVYPTKTFPN 138

RESULT 3
PCT-US95-06613-36
; Sequence 36, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIEFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRY; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
```

REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:

LENGTH: 788
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown

MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:

ORGANISM: Human
STRAIN:

INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:

HAPLOTYPE:
TISSUE TYPE:

CELL TYPE: teratocarcinoma
CELL LINE: N-tera 2D1
ORGANELLE:

FEATURE:
NAME/KEY:

LOCATION:
IDENTIFICATION METHOD:

OTHER INFORMATION: N-tera 2D1 putative
OTHER INFORMATION: APX protein sequence
PCT-US95-06613-36

Query Match 100.0%; Score 76; DB 5; Length 788;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVPTKTFPN 13

Db 126 YMRPVPTKTFPN 138

RESULT 4

US-08-346-455B-34

Sequence 34, Application US/08346455B
Patent No. 5731167

GENERAL INFORMATION:

APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES

TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND

TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE
CITY: NEW YORK

STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994

CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182

FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:

LENGTH: 829
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown

MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:

ORGANISM: Human
STRAIN:

INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:

HAPLOTYPE:
TISSUE TYPE:

CELL TYPE: Melanoma
CELL LINE: A2058
ORGANELLE:

FEATURE:
NAME/KEY:

LOCATION:
IDENTIFICATION METHOD:

OTHER INFORMATION: Putative protein
OTHER INFORMATION: sequence of A2058 Autotaxin
US-08-346-455B-34

Query Match 100.0%; Score 76; DB 1; Length 829;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVPTKTFPN 13

Db 115 YMRPVPTKTFPN 127

RESULT 5

US-08-977-221-34

Sequence 34, Application US/08977221
Patent No. 6084069

GENERAL INFORMATION:

APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES

TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND

TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE
CITY: NEW YORK

STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/977,221
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 829
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: No
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Melanoma
CELL LINE: A2058
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: Putative protein
OTHER INFORMATION: sequence of A2058 Autotaxin
US-08-977-221-34

Query Match 100.0%; Score 76; DB 3; Length 829;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
Db 115 YMRPVYPTKTFPN 127

RESULT 6
PCT-US95-06613-34
Sequence 34, Application PC/TUS9506613
GENERAL INFORMATION:
APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
APPLICANT: HENRY; MURATA, JUN
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 829
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: No
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Melanoma
CELL LINE: A2058
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: Putative protein
OTHER INFORMATION: sequence of A2058 Autotaxin
PCT-US95-06613-34
Query Match 100.0%; Score 76; DB 5; Length 829;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
Db 115 YMRPVYPTKTFPN 127

RESULT 7
US-08-346-455B-69
Sequence 69, Application US/08346455B
Patent No. 5731167
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE

; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,455B
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: A2058 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-346-455B-69

Query Match 100.0%; Score 76; DB 1; Length 915;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
Db 201 YMRPVYPTKTFPN 213

RESULT 8
US-08-977-221-69
; Sequence 69, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,221
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: A2058 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-977-221-69

Query Match 100.0%; Score 76; DB 3; Length 915;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFPN 13
Db 201 YMRPVYPTKTFPN 213

RESULT 9
PCT-US95-06613-69
; Sequence 69, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRY; MORATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US2
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 915
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: No
FEATURE:
NAME/KEY: A2058 ATX protein
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PCT-US95-06613-69

Query Match 100.0%; Score 76; DB 5; Length 915;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
Db 201 YMRPVYPTKTFPN 213

RESULT 10
US-08-346-455B-38
; Sequence 38, Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346.455B
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613

FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 979
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: No
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE: Liver
CELL TYPE:
CELL LINE:
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: putative autotoxin
OTHER INFORMATION: protein sequence from human liver
US-08-346-455B-38

Query Match 100.0%; Score 76; DB 1; Length 979;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
Db 201 YMRPVYPTKTFPN 213

RESULT 11
US-08-977-221-38
; Sequence 38, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1

;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/977,221
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/346,455
;; FILING DATE: 28-NOV-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/249,182
;; FILING DATE: 25-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/822,043
;; FILING DATE: 17-JAN-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DOROTHY R. AUTH
;; REGISTRATION NUMBER: 36,434
;; REFERENCE/DOCKET NUMBER: 2026-4149US3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; INFORMATION FOR SEQ ID NO: 38:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 979
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: Unknown
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Human
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE: Liver
;; CELL TYPE:
;; CELL LINE:
;; ORGANELLE:
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: putative autotoxin
;; OTHER INFORMATION: protein sequence from human liver
;;
US-08-977-221-38

Query Match 100.0%; Score 76; DB 3; Length 979;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
| | | | | | | | | | | | | | | | | |
Db 201 YMRPVYPTKTFPN 213

RESULT 12
PCT-US95-06613-38
; Sequence 38, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRY; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.

;;
;; ZIP: 10154
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy Disk
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/06613
;; FILING DATE: 24-MAY-1995
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/346,455
;; FILING DATE: 28-NOV-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/249,182
;; FILING DATE: 25-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/822,043
;; FILING DATE: 17-JAN-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DOROTHY R. AUTH
;; REGISTRATION NUMBER: 36,434
;; REFERENCE/DOCKET NUMBER: 2026-4149US2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; INFORMATION FOR SEQ ID NO: 38:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 979
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: Unknown
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Human
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE: Liver
;; CELL TYPE:
;; CELL LINE:
;; ORGANELLE:
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: putative autotoxin
;; OTHER INFORMATION: protein sequence from human liver
;;
PCT-US95-06613-38

Query Match 100.0%; Score 76; DB 5; Length 979;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
| | | | | | | | | | | | | | | | | |
Db 201 YMRPVYPTKTFPN 213

RESULT 13
US-08-346-455B-67
; Sequence 67, Application US/08346455B
; Patent No. 5731167
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA; DEPT.
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 861
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: N-tera 2D1 ATX protein
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PS-08-346-455B-67

Query Match 93.4%; Score 71; DB 1; Length 861;
Best Local Similarity 92.3%; Pred. No. 0.00079;
Matches 12; Conservative 1; Mismatches 0; Indels

```
QY      1 YMRPVYPTKTFPN 13
          :|||||
Db     201 HMRPVYPTKTFPN 213
```

```

RESULT 14
US-08-977-221-67
; Sequence 67, Application US/08977221
; Patent No. 6084069
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA
; APPLICANT: OF HEALTH AND HUMAN SERVICES
; TITLE OF INVENTION: MOTILITY STIMULANT
; TITLE OF INVENTION: PROTEIN USEFUL IN THERAPY
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK

```

COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,221
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 20726-4149US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 861
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: N-tera 2D1 ATX protein
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-977-221-67

Query Match 93.4%; Score 71; DB 3; Length 861;
Best Local Similarity 92.3%; Pred. No. 0.00079;
Matches 12; Conservative 1; Mismatches 0; Indels

QY 1 YMRPVYPTKTFPN 13
:|||||
Db 201 HMRPVYPTKTFPN 213

```

RESULT 15
PCT-US95-06613-67
; Sequence 67, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE:
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
; APPLICANT: HENRY; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible

```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06613
; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; REFERENCE/DOCKET NUMBER: 2026-4149US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: N-tera 2D1 ATX protein
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
PCT-US95-06613-67
```

```
Query Match 93.4%; Score 71; DB 5; Length 861;
Best Local Similarity 92.3%; Pred. No. 0.00079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy. 1 VMRPVPTKTFN 13
Db 201 HMRPVPTKTFN 213
:|||||
```

Search completed: July 23, 2001, 13:22:06
Job time: 359 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2001, 14:45:54 ; Search time 25.97 Seconds
(without alignments)
38.131 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213

Perfect score: 76

Sequence: 1 YMRPVYPTKTFPN 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	915	1 A55144	autotaxin precursor
2	70	92.1	885	1 A55453	plasma cell membra
3	69	90.8	96	2 A25274	phosphodiesterase
4	69	90.8	300	2 A41179	protein kinase PC-
5	69	90.8	925	1 A39216	plasma cell membra
6	66	86.8	905	1 A27410	cell surface antig
7	65	85.5	875	1 A57080	hypothetical prote
8	54	71.1	493	2 S50443	hypothetical prote
9	50	65.8	743	2 S19437	hypothetical prote
10	49	64.5	457	2 T09932	nucleotide pyropho
11	49	64.5	461	2 T09933	nucleotide pyropho
12	49	64.5	829	2 T19494	hypothetical prote
13	48	63.2	496	2 T09931	nucleotide pyropho
14	47	61.8	479	2 T03293	nucleotide pyropho
15	45	59.2	674	2 T19495	hypothetical prote
16	44.5	58.6	316	2 S6237	glucan endo-1,3-be
17	42	55.3	429	2 T32514	hypothetical prote
18	41	53.9	247	2 T32514	hypothetical prote
19	41	53.9	381	2 T23250	hypothetical prote
20	41	53.9	427	2 S57776	cysteine proteinas
21	41	53.9	433	2 B82537	phosphodiesterase-
22	41	53.9	493	2 T01206	cysteine proteinas
23	41	53.9	1829	2 T24583	hypothetical prote
24	40	52.6	174	2 S15391	crustacyanin chain
25	40	52.6	205	2 G01942	mitotic feedback c
26	40	52.6	247	2 T45847	hypothetical prote
27	40	52.6	346	2 JAO159	cysteine proteinas
28	40	52.6	466	2 T06416	cysteine proteinas
29	40	52.6	1547	2 JQ0096	hypothetical 176K

```

30 39 51.3 269 2 A84841 probable embryo-ab
31 39 51.3 321 2 E86423 hypothetical prote
32 39 51.3 453 2 T16795 hypothetical prote
33 39 51.3 471 2 G69809 aminoacid carrier
34 39 51.3 485 2 T40657 probable phosphodie
35 39 51.3 528 2 F64580 hypothetical prote
36 39 51.3 528 2 F71931 outer membrane pro
37 39 51.3 1064 2 S52687 serine/threonine-s
38 38 50.0 256 2 T49254 Myb DNA binding pr
39 38 50.0 453 2 S67089 hypothetical prote
40 38 50.0 567 2 C72698 hypothetical prote
41 38 50.0 604 2 S24760 hydroxymethylgluta
42 38 50.0 708 2 T48022 hypothetical prote
43 38 50.0 791 2 T39924 hypothetical prote
44 38 50.0 1068 2 E81965 probable outer mem
45 38 50.0 1082 2 H81020 serotype-I-specifi

```

ALIGNMENTS

RESULT 1

```

A55144
autotaxin precursor - human
N:Contains: phosphodiesterase I (EC 3.1.4.1)
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A55144; A42329
R:Murata, J.; Lee, H.Y.; Clair, T.; Krutzsch, H.C.; Arestad, A.A.; Sobel, M.E.; Liott
J. Biol. Chem. 269, 30479-30484, 1994
A:Title: cDNA cloning of the human tumor motility-stimulating protein, autotaxin, rev
A:Reference number: A55144; MUID:95074054
A:Accession: A55144
A:Molecule type: mRNA
A:Residues: 1-915 <MUR>
A:Cross-references: GB:I35594; NID:9537905; PIDN:AAA64785.1; PID:9537906
A:Note: parts of this sequence were confirmed by peptide sequencing
R:Stracke, M.L.; Krutzsch, H.C.; Unsworth, E.J.; Arestad, A.; Cloce, V.; Schiffmann,
J. Biol. Chem. 267, 2524-2529, 1992
A:Title: Identification, purification, and partial sequence analysis of autotaxin, a
A:Reference number: A42329; MUID:92129337
A:Accession: A42329
A:Molecule type: protein
A:Residues: 256-266;422-444;504-507,'AN',510,'X',511-515;533-548,'S',554-559,'N',561-
A:Experimental source: A2058 melanoma cells
A:Note: sequence extracted from NCBI backbone (NCBIP:78526, NCBIP:78523, NCBIP:78521,
A:Note: a peptide fragment Tyr-Asp-Val-Pro-Trp-Asn-Glu-Thr-Ile was also found
C:Comment: This protein acts as an autocrine factor to stimulate tumor cell motility.
C:Genetics:
A:Gene: GDB:ATX
A:Cross-references: GDB:378346
A:Map position: 8q22-8qter
C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C:Keywords: EF hand; glycoprotein; phosphoprotein; phosphoric diester hydrolase
F:55-98/Domain: somatomedin B homology <SBH1>
F:99-142/Domain: somatomedin B homology <SBH2>
F:54,463,577,859/Binding site: carboxylate (Asn) (covalent) #status predicted
F:210/Binding site: AMP (Thr) (covalent) #status predicted

```

Query Match 100.0%; Score 76; DB 1; Length 915;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13

DB 201 YMRPVYPTKTFPN 213

RESULT 2

```

A55453
plasma cell membrane glycoprotein PC-1, brain specific - rat
N:Contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1)

```

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C:Accession: A55453; JU0187
 R:Narita, M.; Goji, J.; Nakamura, H.; Sano, K.
 J. Biol. Chem. 269, 28235-28242, 1994
 A:Title: Molecular cloning, expression, and localization of a brain-specific phosphodiesterase
 A:Reference number: A55453; MUID:95050605
 A:Accession: A55453
 A:Molecule type: mRNA
 A:Residues: 1-885 <NAR>
 A:Cross-references: GB:D28560; NID:g464196; PIDN:BRA05910.1; PID:g464197
 R:Narita, M.; Goji, J.; Sano, K.; Nakamura, H.
 submitted to JIPID, February 1994
 A:Description: Cloning and expression of brain-specific nucleotide diphosphohydrolase.
 A:Reference number: JU0187
 A:Accession: JU0187
 A:Molecule type: mRNA
 A:Residues: 1-66, 'Q', 68-81, 'T', 83-94, 'C', 96, 'A', 98-195, 'A', 197-514, 'E', 516-621, 'E', 623-6
 A:Experimental source: strain Sprague-Dawley
 C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology
 C:Keywords: coenzyme A; exonuclease; glycoprotein; phosphoprotein; phosphoric diester hyd
 F:54-97/Domain: somatomedin B homology <SBH1>
 F:98-141/Domain: somatomedin B homology <SBH2>
 F:53,150,396,408,522,608,829/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:207/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 92.1%; Score 70; DB 1; Length 885;
 Best Local Similarity 92.3%; Pred. No. 0.00058;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 I | | | | | | | | | |
 Db 198 YTRPVYPTKTFPN 210

RESULT 3
 A25274
 phosphodiesterase I (EC 3.1.4.1) - bovine (fragments)
 N:Alternate names: 5'-exonuclease
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 21-May-1988 #sequence_revision 23-Mar-1995 #text_change 21-May-1999
 C:Accession: A25274; A48395; A48395; D48395
 R:Culp, J.S.; Blytt, H.J.; Hermodson, M.; Butler, L.G.
 J. Biol. Chem. 260, 8320-8324, 1985
 A:Title: Amino acid sequence of the active site peptide of bovine intestinal 5'-nucleoti
 A:Reference number: A25274; MUID:85234541
 A:Accession: A25274
 A:Molecule type: protein
 A:Residues: 1-61 <CU>
 R:Maruyama, E.; Iwamatsu, A.; Takashima, S.
 Biochem. Mol. Biol. Int. 29, 579-586, 1993
 A:Title: Purification and amino acid microsequencing of alkaline phosphodiesterase I fr
 A:Reference number: A48395; MUID:93250579
 A:Accession: A48395
 A:Molecule type: protein
 A:Residues: 22-36,62-73;74-81;82-96 <MAR>
 A:Experimental source: kidney
 A:Note: sequence extracted from NCBI backbone (NCBI:P132415, NCBI:P131478)
 A:Note: the correct order of the fragments is unknown
 C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology
 C:Keywords: phosphoprotein; phosphoric diester hydrolase
 F:33/Binding site: AMP (Thr) (covalent) #status experimental

Query Match 90.8%; Score 69; DB 2; Length 96;
 Best Local Similarity 84.6%; Pred. No. 9.1e-05;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 I | | | | | | | | | |
 Db 30 YLRPAVPTKTFPN 42

RESULT 4
 A41179
 protein kinase PC-1 (EC 2.7.1.1) - bovine (fragments)
 N:Alternate names: MAPK; major acidic fibroblast growth factor-stimulated phosphoprot
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 28-May-1992 #sequence_revision 22-Apr-1995 #text_change 30-Apr-1999
 C:Accession: A41179; A49308
 R:Oda, Y.; Kuo, M.D.; Huang, S.S.; Huang, J.S.
 J. Biol. Chem. 266, 16791-16795, 1991
 A:Title: The plasma cell membrane glycoprotein, PC-1, is a threonine-specific protein
 A:Reference number: A41179; MUID:91358477
 A:Accession: A41179
 A:Molecule type: protein
 A:Residues: 1-26;36-56;59-67;68-133;134-144;145-267;268-300 <ODA>
 A:Experimental source: liver
 R:Oda, Y.; Kuo, M.D.; Huang, S.S.; Huang, J.S.
 J. Biol. Chem. 268, 27318-27326, 1993
 A:Title: The major acidic fibroblast growth factor (aFGF)-stimulated phosphoprotein f
 esterase activities.
 A:Reference number: A49308; MUID:94086550
 A:Accession: A49308
 A:Molecule type: protein
 A:Residues: 27-35, 'X', 37-58 <OD2>
 A:Experimental source: liver
 A:Note: sequence extracted from NCBI backbone (NCBI:P141583)
 C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology
 C:Keywords: glycoprotein; phosphoprotein; phosphotransferase
 F:1-23/Domain: somatomedin B homology (fragment) <SBH>
 F:36/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 90.8%; Score 69; DB 2; Length 300;
 Best Local Similarity 100.0%; Pred. No. 0.00029;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVYPTKTFPN 13
 I | | | | | | | | | |
 Db 28 MRPVYPTKTFPN 39

RESULT 5
 A39216
 plasma cell membrane glycoprotein PC-1 - human
 N:Contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1)
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-May-2000
 C:Accession: A39216; S21706; S23587; S51030
 R:Buckley, M.F.; Loveland, K.A.; McKinstry, W.J.; Garson, O.M.; Goding, J.W.
 J. Biol. Chem. 265, 17506-17511, 1990
 A:Title: Plasma cell membrane glycoprotein PC-1. cDNA cloning of the human molecule,
 A:Reference number: A39216; MUID:91009202
 A:Accession: A39216
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-925 <BUC>
 A:Cross-references: GB:J05654
 R:Funakoshi, I.; Kato, H.; Horie, K.; Yano, T.; Hori, Y.; Kobayashi, H.; Inoue, T.; S
 Arch. Biochem. Biophys. 295, 180-187, 1992
 A:Title: Molecular cloning of cDNAs for human fibroblast nucleotide pyrophosphatase.
 A:Reference number: S21706; MUID:92246539
 A:Accession: S21706
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-925 <FUN1>
 A:Accession: S23587
 A:Molecule type: protein
 A:Residues: 116-121,247-271, 'X', 273-275;279-280, 'X', 282-283;303-316;362-364;449-465;4
 A:Note: it is uncertain whether Met-1 or Met-53 is the Initiator
 R:Beili, S.I.; Goding, J.W.
 Eur. J. Biochem. 226, 433-443, 1994
 A:Title: Biochemical characterization of human PC-1, an enzyme possessing alkaline ph

A:Reference number: S51030; MUID:95094801

A:Accession: S51030

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-80 <BEL>

C:Genetics:

A:Gene: GDB:PDNPL1; MGS1; NPFS

A:Cross-references: GDB:I32615; OMIM:173335

A:Map position: 6q22-6q23

C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology

C:Keywords: coenzyme A; glycoprotein; phosphoprotein; phosphoric diester hydrolase; transmembrane #status predicted <TM>

F:77-97/Domain: transmembrane #status predicted <TM>

F:104-144/Domain: somatomedin B homology <SBH1>

F:145-188/Domain: somatomedin B homology <SBH2>

F:179-285/Domain: somatomedin B homology (covalent) #status predicted

F:256/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 90.8%; Score 69; DB 1; Length 925;

Best Local Similarity 100.0%; Pred. No. 0.0009;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVPTKTFPN 13

|||||

DB 248 MRPVPTKTFPN 259

RESULT 6

A27410 plasma cell membrane glycoprotein PC-1 - mouse

A:Alternate names: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.1.1)

C:Species: Mus musculus (house mouse)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-May-2000

C:Accession: A27410; I59055; S38354

R:van Driel, I.R.; Goding, J.W.

J. Biol. Chem. 262, 4882-4887, 1987

A:Title: Plasma cell membrane glycoprotein PC-1. Primary structure deduced from cDNA cloning

A:Reference number: A27410; MUID:87165906

A:Accession: A27410

A:Molecule type: mRNA

A:Residues: 1-905 <VAN>

A:Cross-references: GB:J02700; NID:g200236; PIDN:AAA39893.1; PID:g200237

A:Note: the authors translated the codon CAG for residue 24 as Glu

R:van Driel, I.R.; Wilks, A.F.; Pietersz, G.A.; Goding, J.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 8619-8623, 1985

A:Title: Murine plasma cell membrane antigen PC-1: Molecular cloning of cDNA and analysis

A:Reference number: I59055; MUID:86094275

A:Accession: I59055

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 203-219 <RES>

A:Cross-references: GB:M12552; NID:g200234; PIDN:AAA39892.1; PID:g200235

R:Belli, S.I.; van Driel, I.R.; Goding, J.W.

Eur. J. Biochem. 217, 421-428, 1993

A:Title: Identification and characterization of a soluble form of the plasma cell membrane

A:Reference number: S38354; MUID:94039066

A:Accession: S38354

A:Molecule type: DNA

A:Residues: 35-219 <BEL>

A:Cross-references: EMBL:L04516

C:Genetics:

A:Introns: 62/3; 87/1; 126/1; 188/2

C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology

C:Keywords: coenzyme A; glycoprotein; phosphoprotein; phosphoric diester hydrolase; transmembrane #status predicted <TM>

F:86-126/Domain: somatomedin B homology <SBH1>

F:127-170/Domain: somatomedin B homology <SBH2>

F:161,267,323,459,567,624/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:238/Binding site: AMP (Thr) (covalent) #status predicted

Query Match

Best Local Similarity 86.8%; Score 66; DB 1; Length 905;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVPTKTFPN 13
|||||

DB 230 MRPVPTKTFPN 241

RESULT 7

A57080

cell surface antigen RBL3-6 - rat

N:Contains: phosphodiesterase I (EC 3.1.1.4.1)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A57080

R:Deissler, H.; Lottspeich, F.; Rajewsky, M.F.

J. Biol. Chem. 270, 9849-9855, 1995

A:Title: Affinity purification and cDNA cloning of rat neural differentiation and tum

A:Reference number: A57080; MUID:95247775

A:Accession: A57080

A:Molecule type: mRNA

A:Residues: 1-875 <DEI>

A:Cross-references: GB:Z47987; NID:g806378; PIDN:CAA88029.1; PID:g806379

C:Superfamily: nucleotide pyrophosphatase; somatomedin B homology

C:Keywords: exonuclease; glycoprotein; phosphoprotein; phosphoric diester hydrolase;

F:1-22/Domain: cytosolic #status predicted <CYT>

F:23-45/Domain: transmembrane #status predicted <TM>

F:46-875/Domain: extracellular #status predicted <EXT>

F:51-94/Domain: somatomedin B homology <SBH>

F:95-138/Domain: somatomedin B homology <SBH2>

F:206/Binding site: AMP (Thr) (covalent) #status predicted

F:237,280,289,533,574,594,702,789/Binding site: carbohydrate (Asn) (covalent) #status

Query Match 85.5%; Score 65; DB 1; Length 875;

Best Local Similarity 84.6%; Pred. No. 0.0041;

Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVPTKTFPN 13

|||||

DB 197 YMRPVPTKTFPN 209

RESULT 8

S50443

hypothetical protein YEL016c - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 29-Oct-1999

C:Accession: S50443

R:Dietrich, F.S.

submitted to the EMBL Data Library, December 1994

A:Description: Saccharomyces cerevisiae chromosome V cosmids 9871, 8199, 9867, 9495 a

A:Reference number: S50428

A:Accession: S50443

A:Molecule type: DNA

A:Residues: 1-493 <DIE>

A:Cross-references: EMBL:U18530; NID:g602367; PID:g602383; GSPDB:GN00005; MIPS:YEL016

C:Genetics:

A:Gene: MIPS:YEL016c

A:Map position: 5L

Query Match

Best Local Similarity 71.1%; Score 54; DB 2; Length 493;

Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YMRPVPTKTFPN 13

|||||

DB 118 YMRPVPTKTFPN 130

RESULT 9

S19437

hypothetical protein YCR026c - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: Hypothetical protein YCR247
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 12-Dec-1997
 C:Accession: S19437; S19750; S27380
 R:Poln, F.; Richterich, P.; Wurst, H.
 submitted to the Protein Sequence Database, March 1992
 A:Reference number: S19437
 A:Accession: S19437
 A:Molecule type: DNA
 A:Residues: 1-244 <FOH>
 A:Cross-references: EMBL:X59720; MIPS:YCR026c
 R:Berben, G.; Bolle, P.A.; Gilliquet, V.; Hilger, F.
 submitted to the Protein Sequence Database, March 1992
 A:Reference number: S19433
 A:Accession: S19750
 A:Molecule type: DNA
 A:Residues: 244-743 <BER>
 A:Cross-references: EMBL:X59720; MIPS:YCR026c
 R:Berben, G.; Bolle, P.A.; Gilliquet, V.; Berben, G.; Dumont, J.; Hilger, F.
 Yeast 8, 205-213, 1992
 A:Title: The complete sequence of K3B, a 7.9 kb fragment between PGK1 and CRY1 on chromosome 1
 A:Reference number: S22273; MUID:92245758
 A:Accession: S27380
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-106, 'H', 108-119, 'F', 121-211, 'V', 213-743 <BOL>
 C:Genetics:
 A:Map position: 3R
 C:Keywords: transmembrane protein

Query Match 65.8%; Score 50; DB 2; Length 743;
 Best Local Similarity 61.5%; Pred. No. 1.2;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 : : : : :
 Db 210 FMPSFTETFPN 222

RESULT 10
 T09932
 nucleotide pyrophosphatase homolog T16L4.200 - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
 C:Accession: T09932
 R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, June 1999
 A:Reference number: Z16897
 A:Accession: T09932
 A:Molecule type: DNA
 A:Residues: 1-457 <BEV>
 A:Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.200
 A:Experimental source: cultivar Columbia; BAC clone T16L4
 C:Genetics:
 A:Gene: ATSP:T16L4.200
 A:Map position: 4

Query Match 64.5%; Score 49; DB 2; Length 457;
 Best Local Similarity 80.0%; Pred. No. 1.1;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PVYPTKTFPN 13
 : : : : :
 Db 94 PVFTMTFPN 103

RESULT 11
 T09933
 nucleotide pyrophosphatase homolog T16L4.210 - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
 C:Accession: T09933
 R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.
 submitted to the Protein Sequence Database, June 1999
 A:Reference number: Z16897
 A:Accession: T09933
 A:Molecule type: DNA
 A:Residues: 1-461 <BEV>
 A:Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.210
 A:Experimental source: cultivar Columbia; BAC clone T16L4
 C:Genetics:
 A:Gene: ATSP:T16L4.210
 A:Map position: 4

Query Match 64.5%; Score 49; DB 2; Length 461;
 Best Local Similarity 80.0%; Pred. No. 1.1;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PVYPTKTFPN 13
 : : : : :
 Db 97 PVFTMTFPN 106

RESULT 12
 T19494
 hypothetical protein C27A7.1 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T19494
 R:Harris, B.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19132
 A:Accession: T19494
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-829 <WIL>
 A:Cross-references: EMBL:Z81041; PIDN:CAB02784.1; GSPDB:GN00023; CESP:C27A7.1
 A:Experimental source: clone C27A7
 C:Genetics:
 A:Gene: CESP:C27A7.1
 A:Map position: 5
 A:Introns: 12/3; 37/1; 100/3; 176/2; 272/3; 392/1; 427/1; 479/2; 566/2; 588/3; 677/1;

Query Match 64.5%; Score 49; DB 2; Length 829;
 Best Local Similarity 80.0%; Pred. No. 2;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PVYPTKTFPN 13
 : : : : :
 Db 218 PSYPTKTFPN 227

RESULT 13
 T09931
 nucleotide pyrophosphatase homolog T16L4.190 - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
 C:Accession: T09931
 R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.
 submitted to the Protein Sequence Database, June 1999
 A:Reference number: Z16897
 A:Accession: T09931
 A:Molecule type: DNA
 A:Residues: 1-496 <BEV>
 A:Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.190
 A:Experimental source: cultivar Columbia; BAC clone T16L4
 C:Genetics:
 A:Gene: ATSP:T16L4.190
 A:Map position: 4

Query Match 63.2%; Score 48; DB 2; Length 496;
Best Local Similarity 80.0%; Pred. No. 1.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PVYPTKTFPN 13
|:|:|:|:|:|
Db 146 PVFPTLTFFN 155

RESULT 14

T03293
nucleotide pyrophosphatase homolog - rice
C:Species: Oryza sativa (rice)
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C:Accession: T03293
R:Hsing, Y.C.; Tsao, C.V.; Chow, T.; Hsieh, J.; Chen, Z.
submitted to the EMBL Data Library, April 1995
A:Description: Rice early embryogenesis gene.
A:Reference number: Z14889
A:Accession: T03293
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-479 <HSI>
A:Cross-references: EMBL:U25430; NID:g818848; PID:g818849
A:Experimental source: strain Tainung 67
C:Genetics:
A:Note: OSE4

Query Match 61.8%; Score 47; DB 2; Length 479;
Best Local Similarity 70.0%; Pred. No. 2.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PVYPTKTFPN 13
|:|:|:|:|:|
Db 129 PIFPTLTFFN 138

RESULT 15

T19495
hypothetical protein C27A7.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19495
R:Harris, B.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19132
A:Accession: T19495
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-674 <WIL>
A:Cross-references: EMBL:Z81041; PIDN:CAB02785.1; GSPDB:GN00023; CESP:C27A7.3
A:Experimental source: clone C27A7
C:Genetics:
A:Gene: CESP:C27A7.3
A:Map position: 5
A:Introns: 61/1; 98/3; 191/1; 220/3; 268/3; 340/1; 392/2; 475/2; 496/3; 537/1; 588/1

Query Match 59.2%; Score 45; DB 2; Length 674;
Best Local Similarity 70.0%; Pred. No. 7.7;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PVYPTKTFPN 13
|:|:|:|:|:|
Db 166 PSFPTKTFPN 175

Search completed: July 19, 2001, 14:45:55
Job time: 153 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:47:09 ; Search time 16.91 seconds
(without alignments)

26.335 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213

Perfect score: 76

Sequence: 1 YMRPVYPTKTFPN 13

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	90.8	61	1	PPD1_BOVIN
2	69	90.8	873	1	PC1_HUMAN
3	66	86.8	871	1	PC1_MOUSE
4	54	71.1	493	1	YEB6_YEAST
5	50	65.8	743	1	YCR6_YEAST
6	44.5	58.6	316	1	E13E_HORVU
7	42	55.3	743	1	BGAL_THEET
8	40	52.6	174	1	CRA2_HOMGA
9	40	52.6	205	1	MD21_HUMAN
10	40	52.6	205	1	MD21_MOUSE
11	40	52.6	346	1	MD21_LYCES
12	40	52.6	1547	1	RRPO_PMV
13	39	51.3	595	1	HMD2_SOLTU
14	39	51.3	890	1	YCF2_MESVI
15	39	51.3	1064	1	KIN1_YEAST
16	38	50.0	172	1	CH18_DROME
17	38	50.0	604	1	HMDH_NICSY
18	37	48.7	177	1	CRAB_SQUAC
19	37	48.7	232	1	HB23_MOUSE
20	37	48.7	264	1	HB21_MOUSE
21	37	48.7	264	1	HB22_MOUSE
22	37	48.7	264	1	HB24_MOUSE
23	37	48.7	264	1	HB21_MOUSE
24	37	48.7	264	1	HB21_MOUSE
25	37	48.7	328	1	GPT_SULAC
26	37	48.7	333	1	PAP2_VACCC
27	37	48.7	333	1	PAP2_VACCV
28	37	48.7	333	1	PAP2_MARY
29	37	48.7	480	1	SYFA_METJA
30	37	48.7	602	1	HMD2_LYCES
31	37	48.7	636	1	UBA2_YEAST
32	37	48.7	3358	1	PCGV_MOUSE
33	37	48.7	3866	1	HRX_MOUSE

34	37	48.7	3969	1	HRX_HUMAN	Q03164	homo sapien
35	36.5	48.0	910	1	SC15_YEAST	P22224	saccharomyc
36	36	47.4	210	1	THIE_ARCFU	O28205	archaeoglob
37	36	47.4	305	1	GP7D_CHLTR	P10561	chlamydia t
38	36	47.4	716	1	BGAL_THETU	P26257	thermoanaer
39	36	47.4	750	1	FOH1_HUMAN	Q04609	homo sapien
40	35.5	46.7	863	1	APCE_CYACA	P35911	cyanidium c
41	35.5	46.7	883	1	APCE_CYAPA	P48088	cyanophora
42	35	46.1	222	1	THIE_BACSU	P39534	bacillus su
43	35	46.1	278	1	TONB_NEIMC	P95374	neisseria m
44	35	46.1	280	1	TONB_NEIMA	P37003	neisseria m
45	35	46.1	280	1	TONB_NEIMB	P57004	neisseria m

ALIGNMENTS

```
RESULT 1
PPD1_BOVIN
ID PPD1_BOVIN STANDARD; PRT; 61 AA.
AC P15396;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-NUCLEOTIDE
DE PHOSPHODIESTERASE) (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=85234541; PubMed=2989287;
RA Culp J.S., Blytt H.J., Hermanson M., Butler L.G.;
RT "Amino acid sequence of the active site peptide of bovine intestinal
RT 5'-nucleotide phosphodiesterase and identification of the active
RT site residue as threonine."
RL J. Biol. Chem. 260:8320-8324(1985).
CC -I- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
CC SUCCESSFULLY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
CC OLIGO-NUCLEOTIDES.
CC PIR; A25274; A25274.
KW Hydrolase.
FT NON_TER 1. 1
FT ACT_SITE 39. 39 FORMS A PHOSPHOTREONINE INTERMEDIATE.
SQ SEQUENCE 61 AA; 6999 MW; 580C8B4807A61C84 CRC64;
```

Query Match 90.8%; Score 69; DB 1; Length 61;
Best Local Similarity 84.6%; Pred. No. 1.9e-05;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
DB 30 YLRPAYPTKTFPN 42

RESULT 2

```
PC1_HUMAN
ID PC1_HUMAN STANDARD; PRT; 873 AA.
AC P22413; Q9Y6K3; Q9UP61;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1 [INCLUDES: ALKALINE
DE PHOSPHODIESTERASE I (EC 3.1.4.1); NUCLEOTIDE PYROPHOSPHATASE
DE (EC 3.6.1.9) (NPPASE)].
GN PDNP1 OR PC1 OR NPPS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DR EMBL: J02700; AAA39893.1; ALT_INIT.
DR EMBL; M12552; AAA39892.1; -
DR PIR; A27410; A27410.
DR MGD; MGI:97370; pdnp1.
DR InterPro; IPR001212; -
DR InterPro; IPR002591; -
DR Pfam; PF01663; Phosphodiester; 1.
DR Pfam; PF01033; Somatomedin_B; 2.
DR PRINTS; PR00022; Somatomedin_B.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
KW Glycoprotein; Transmembrane; BLOCKED; Signal-anchor; Hydrolase.
FT MOD_RES ?1 ?1
FT DOMAIN 1 24 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 25 45 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 46 871 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 52 92 SOMATOMEDIN-B LIKE.
FT DOMAIN 93 136 SOMATOMEDIN-B LIKE.
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 533 533 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 590 590 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 871 AA; 99487 MW; 80848F81071F70AA CRC64;

Query Match 86.8%; Score 66; DB 1; Length 871;
Best Local Similarity 91.7%; Pred. No. 0.001;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVYPTKTFPN 13
|||:|||||||
DB 196 MRPVYPTKTFPN 207

RESULT 4
ID YEB6_YEAST STANDARD; PRT; 493 AA.
AC P39997;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HYPOTHETICAL 57.4 KDA PROTEIN IN PMP2-VAC8 INTERGENIC REGION.
GN YEL016C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Berio A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Hunnicke-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO YEAST YCR26C.

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CC EMBL; U18530; AAB64493.1; -
CC SGD: S0000742; YEL016C.
DR InterPro; IPR002591; -
DR Pfam; PF01663; Phosphodiester; 1.
KW Hypothetical protein.
SQ SEQUENCE 493 AA; 57354 MW; 10E67A05C6DEDF09 CRC64;

Query Match 71.1%; Score 54; DB 1; Length 493;
Best Local Similarity 69.2%; Pred. No. 0.063;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
|||:|||||
DB 118 YMFSPFTTFPN 130

RESULT 5
ID YCR6_YEAST STANDARD; PRT; 743 AA.
AC P25353;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HYPOTHETICAL 84.9 KDA PROTEIN IN PMP1-FEN2 INTERGENIC REGION.
GN YCR026C OR YCR26C OR YCR246.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE OF 1-244 FROM N.A.
RA Pohl F., Richterich P., Wurst H.;
RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 244-743 FROM N.A.
RA MEDLINE=92245758; PubMed=1574926;
RA Bolle P.-A., Gilliquet V., Berben G., Dumont J., Hilger F.;
RT "The complete sequence of K3B, a 7.9 kb fragment between PGK1 and
RT CRY1 on chromosome III, reveals the presence of seven open reading
RT frames."
RL Yeast 8:205-213(1992).
CC -1- SIMILARITY: TO YEAST YEL016C.

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DR EMBL: X59720; CAA42318.1; -
DR PIR; S19437; S19437.
DR PIR; S27380; S27380.
DR SGD: S0000621; YCR026C.
DR InterPro; IPR002591; -
DR Pfam; PF01663; Phosphodiester; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 114 135 POTENTIAL.
SQ SEQUENCE 743 AA; 84915 MW; 2385E9F4BA948B0D CRC64;

Query Match 65.8%; Score 50; DB 1; Length 743;
Best Local Similarity 61.5%; Pred. No. 0.47; Indels 0; Gaps 0;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
|||:|||||
DB 210 FMPSFPTTFPN 222

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RESULT 6
E13E_HORVU STANDARD; PRT; 316 AA.
ID Q02438;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE GLUCAN ENDO-1,3-BETA-GLUCOSIDASE GV (EC 3.2.1.39) ((1->3)-BETA-GLUCAN
DE ENDOHYDROLASE GV) ((1->3)-BETA-GLUCANASE ISOENZYME GV) (BETA-1,3-
DE ENDOGLUCANASE GV).
OS Hordeum vulgare (barley).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae;
OC Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, CLIPPER; TISSUE=Root, and Leaf;
RX MEDLINE=94307426; PubMed=8034043;
RA Xu P., Harvey A.J., Fincher G.B.;
RT "Heterologous expression of cDNAs encoding barley (Hordeum vulgare)
RT (1->3)-beta-glucanase isoenzyme GV.";
RL FEBS Lett. 348:206-210(1994).
RN [2]
RP SEQUENCE OF 5-316 FROM N.A.
RC STRAIN=CV, CLIPPER; TISSUE=Root, and Leaf;
RX MEDLINE=93013030; PubMed=1398132;
RA Xu P., Wang J., Fincher G.B.;
RT "Evolution and differential expression of the (1->3)-beta-glucan
RT endohydrolase-encoding gene family in barley, Hordeum vulgare.";
RL Gene 120:157-165(1992).
CC -1- FUNCTION: MAY PROVIDE A DEGREE OF PROTECTION AGAINST MICROBIAL
CC INVASION OF GERMINATED BARLEY GRAIN THROUGH ITS ABILITY TO DEGRADE
CC FUNGAL CELL WALL POLYSACCHARIDES.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,3-BETA-D-GLUCOSIDIC LINKAGES
CC IN 1,3-BETA-D-GLUCANS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
CC -1- SIMILARITY: BELONGS TO FAMILY 17 OF GLYCOSYL HYDROLASES.
CC
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CC
CC EMBL; M96939; AAA21564.1; -.
CC PIR; JC1438; JCI438.
CC HSP; P15737; IGHS.
CC InterPro; IPR000490; -.
CC Pfam; PF00332; Glyco_hydro_17; 1.
CC PROSITE; PS00587; GLYCOSYL_HYDROL_F17; 1.
CC Hydroxylase; Glycosidase; Multigene family.
CC ACT_SITE 239 239 NUCLEOPHILE (BY SIMILARITY).
CC ACT_SITE 296 296 PROTON DONOR (BY SIMILARITY).
CC SEQUENCE 316 AA; 34413 MW; 0CC0RA9DA48269B4F CRC64;

Query Match 58.6%; Score 44.5; DB 1; Length 316;
Best Local Similarity 81.8%; Pred. No. 1.7;
Matches 9; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 3 RPVYPTKTFPN 13
:|||||
DB 307 QPVYPT-TFPN 316

RESULT 7
BGAL_THEET STANDARD; PRT; 743 AA.
ID BGAL_THEET
AC P77989;

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DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE BETA-GALACTOSIDASE (EC 3.2.1.23) (LACTASE).
GN LACZ OR LACA.
OS Thermoanaerobacter ethanolicus (Clostridium thermohydrosulfuricum).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Thermoanaerobacter group; Thermoanaerobacter.
OX NCBI_TaxID=1757;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33223 / 39E;
RA Zverlov V.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-
CC GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
CC
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CC
CC EMBL; Y08557; CAA69850.1; -.
CC InterPro; IPR001649; -.
CC Pfam; PF00703; Glyco_hydro_2; 1.
CC PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; 1.
CC PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; 1.
CC Hydroxylase; Glycosidase.
CC ACT_SITE 388 388 PROTON DONOR (BY SIMILARITY).
CC ACT_SITE 453 453 NUCLEOPHILE (BY SIMILARITY).
CC SEQUENCE 743 AA; 85796 MW; FE01FF517E51DFC CRC64;

Query Match 55.3%; Score 42; DB 1; Length 743;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
:|||||
DB 454 YMGHMTPTKSYDN 466

RESULT 8
CRA2_HOMCA STANDARD; PRT; 174 AA.
ID CRA2_HOMCA
AC P80007;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE CRUSTACEANIN A2 SUBUNIT.
OS Homarus gammarus (European lobster) (Homarus vulgaris).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6707;
RN [1]
RP SEQUENCE.
RX MEDLINE=91224133; PubMed=2026162;
RA Keen J.N., Caceres I., Eliopoulos E.E., Zagalsky P.F.,
RA Findlay J.B.C.;
RT "Complete sequence and model for the A2 subunit of the carotenoid
RT pigment complex, crustacyanin."
RL Eur. J. Biochem. 197:407-417(1991).
CC -1- FUNCTION: BINDS THE CAROTENOID ASTAXANTHIN WHICH PROVIDES THE BLUE
CC COLORATION TO THE CARAPACE OF THE LOBSTER.
CC -1- SUBUNIT: OLIGOMER; CAN FORM DIMERS (BETA-CRUSTACYANIN); OR
CC COMPLEXES OF 16 SUBUNITS (ALPHA-CRUSTACYANIN). THERE ARE FIVE
CC TYPES OF SUBUNITS: A1, A2, A3, C1 AND C2.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR, CARAPACE.

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CC -!- SIMILARITY: BELONGS TO THE LIPOCALIN FAMILY.
DR PIR; S15391; S15391.
DR InterPro; IPR000566; -.
DR InterPro; IPR002345; -.
DR InterPro; IPR003057; -.
DR Pfam; PF00061; lipocalin; 1.
DR PRINTS; PR00179; LIPOCALIN.
DR PRINTS; PR01273; INVTBRTCOLOR.
DR PROSITE; PS00213; LIPOCALIN; 1.
KW Pigment; Lipocalin; Transport.
FT DISULFID 12 119 BY SIMILARITY.
FT DISULFID 46 170 BY SIMILARITY.
SQ SEQUENCE 174 AA; 19670 MW; AC47FAA650C5E44E CRC64;

Query Match 52.6%; Score 40; DB 1; Length 174;
Best Local Similarity 87.5%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 VYPTKTFP 12
|||||
Db 80 VYPTKEFP 87

RESULT 9
MD21_HUMAN STANDARD; PRT; 205 AA.
AC Q13257;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE MITOTIC SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2A (MAD2-LIKE 1)
DE (HSMAD2)
GN MAD2L1 OR MAD2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96421709; PubMed=8824189;
RA Li Y., Benezra R.;
RT "Identification of a human mitotic checkpoint gene: hsmad2.";
RL Science 274:246-248(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Jin D.-Y., Jeang K.-T.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Kleibert S., Barnikol-Watanabe S., Kratzin H.D., Hilschmann N.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP INTERACTION WITH CDC20.
RX MEDLINE=98301442; PubMed=9637688;
RA Fang G., Yu H., Kirschner M.W.;
RT "The checkpoint protein MAD2 and the mitotic regulator CDC20 form a
ternary complex with the anaphase-promoting complex to control
anaphase initiation."
RL Genes Dev. 12:1871-1883(1998).
RN [5]
RP INTERACTION WITH ADAM17.
RX PubMed=10527948;
RA Nelson K.K., Schlondorff J., Blobel C.P.;
RT "Evidence for an interaction of the metalloprotease-disintegrin tumour
necrosis factor alpha convertase (TACE) with mitotic arrest deficient
2 (MAD2), and of the metalloprotease-disintegrin MDC9 with a novel
MAD2-related protein, MAD2-beta."
RL Biochem. J. 343:673-680(1999).
RN [6]
RP STRUCTURE BY NMR OF 11-195.
RX MEDLINE=20165182; PubMed=10700282;
RA Luo X., Fang G., Coldiron M., Lin Y., Yu H., Kirschner M.W.,

Wagner G.;
"Structure of the Mad2 spindle assembly checkpoint protein and its
interaction with Cdc20.";
RL Nat. Struct. Biol. 7:224-229(2000).
CC -!- FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT
WHICH MONITORS THE PROCESS OF KINETOCHORE-SPINDLE ATTACHMENT AND
DELAYS THE ONSET OF ANAPHASE WHEN THIS PROCESS IS NOT COMPLETE. IT
INHIBITS THE ACTIVITY OF THE ANAPHASE PROMOTING COMPLEX BY
SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE
METAPHASE PLATE.
CC -!- SUBUNIT: INTERACTS WITH CDC20 AND WITH ADAM17 (TACE).
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SIMILARITY: BELONGS TO THE MAD2 FAMILY.
-----
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DR EMBL; U65410; AAC50781.1; -.
DR EMBL; U31278; AAC52060.1; -.
DR EMBL; AJ000186; CAA03943.1; -.
DR MIM; 601467; -.
DR PDB; 1D03; O8-MAR-00.
DR InterPro; IPR003511; -.
DR Pfam; PF02301; HORMA; 1.
KW Cell cycle; Mitosis; Nuclear protein; 3D-structure.
SQ SEQUENCE 205 AA; 23510 MW; B8DCBF0043836764 CRC64;

Query Match 52.6%; Score 40; DB 1; Length 205;
Best Local Similarity 54.5%; Pred. No. 6.2;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTF 11
| | | | |
Db 33 YQGIYPSETF 43

RESULT 10
MD21_MOUSE STANDARD; PRT; 205 AA.
ID MD21_MOUSE
AC Q9Z1B5; Q9J153;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE MITOTIC SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2A (MAD2-LIKE 1).
GN MAD2L1 OR MAD2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Embryo;
RA Jin D.-Y., Jeang K.-T.;
RT "Identification of a novel component of the spindle assembly
checkpoint in mammalian cells."
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129;
RX PubMed=10892650;
RA Dobles M., Liberal V., Scott M.L., Benezra R., Sorger P.K.;
RT "Chromosome missegregation and apoptosis in mice lacking the mitotic
checkpoint protein Mad2."
RL Cell 101:635-645(2000).
CC -!- FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT
WHICH MONITORS THE PROCESS OF KINETOCHORE-SPINDLE ATTACHMENT AND
DELAYS THE ONSET OF ANAPHASE WHEN THIS PROCESS IS NOT COMPLETE. IT
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CC INHIBITS THE ACTIVITY OF THE ANAPHASE PROMOTING COMPLEX BY
CC SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE
CC METAPHASE PLATE (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH CDC20.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MAD2 FAMILY.
CC -----
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CC -----
CC EMBL; U83902; AAD09238.1; -
CC EMBL; AF261919; AAF69525.1; -
CC InterPro; IPR003511; -
CC Pfam; PF02301; HORMA; 1.
CC Cell cycle; Mitosis; Nuclear protein.
CC CONFLICT 157 157 T -> A (IN REF. 1).
CC CONFLICT 178 178 C -> S (IN REF. 1).
CC CONFLICT 201 201 T -> I (IN REF. 1).
CC SEQUENCE 205 AA; 23598 MW; A9F3F28BC4C9738E CRC64;
CC -----
Query Match 52.6%; Score 40; DB 1; Length 205;
Best Local Similarity 54.5%; Pred. No. 6.2; Indels 0; Gaps 0;
Matches 6; Conservative 3; Mismatches 2;
CC
QY 1 YMRPVYPTKTF 11
| | :||:|
DB 33 YQGIYPTSETF 43
| | :||:|

RESULT 11
CYSL_LYCES STANDARD; PRT; 346 AA.
AC P20721; 1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE LOW-TEMPERATURE-INDUCED CYSTEINE PROTEINASE PRECURSOR (EC 3.4.22.-)
DE (FRAGMENT).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. VENT CHERRY;
RA Schaffer M.A., Fischer R.L.;
RT "Analysis of mRNAs that accumulate in response to low temperature
RT identifies a thiolprotease in tomato."
RL Plant Physiol. 87:431-436(1988).
CC -1- INDUCTION: IN RESPONSE TO LOW TEMPERATURE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
CC PAPAINE FAMILY OF THIOL PROTEASES.
CC -----
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CC -----
CC EMBL; M21444; AAA66308.1; -
CC PIR; JAO159; JAO159.
CC HSSP; P00785; 2ACT.
CC MEROPS; C01.029; -
CC InterPro; IPR000118; -

DR InterPro; IPR000169; -
DR InterPro; IPR000668; -
DR Pfam; PF00112; Peptidase_C1; 1.
DR Pfam; PF00396; granulin; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE-NEG.
KW Hydrolase; Thiol protease; zymogen; Glycoprotein.
FT NON_TER 1 1
FT PROPEP <1 17
FT CHAIN 18 346
FT -----
FT ACT_SITE 42 42
FT ACT_SITE 178 178
FT ACT_SITE 198 198
FT ACT_SITE 39 81
FT DISULFID 73 114
FT DISULFID 172 223
FT CARBOHYD 215 215
FT SEQUENCE 346 AA; 37429 MW; D42AC73944010928 CRC64;
FT -----
Query Match 52.6%; Score 40; DB 1; Length 346;
Best Local Similarity 58.3%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
CC
QY 2 MRPVYPTKTFPN 13
| | :||:|
DB 227 IEPYVPKTCGN 238
| | :||:|

RESULT 12
RRPO_PMW STANDARD; PRT; 1547 AA.
ID RRPO_PMW
AC P20951;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RNA REPLICATION PROTEIN (176 KDA PROTEIN) (ORF 1) [CONTAINS: RNA-
DE DIRECTED RNA POLYMERASE (EC 2.7.7.48); PROBABLE HELICASE].
OS Papaya mosaic potexvirus (PMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
OX NCBI_TaxID=12181;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89381685; PubMed=2778435;
RA Sit T.L., Abouhaider M.G., Holy S.;
RT "Nucleotide sequence of papaya mosaic virus RNA."
RL J. Gen. Virol. 70:2325-2331(1989).
CC -1- FUNCTION: RNA-REPLICATION. THE CENTRAL PART OF THIS PROTEIN
CC POSSIBLY FUNCTIONS AS A ATP-BINDING HELICASE.
CC -----
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CC -----
CC EMBL; D13957; BAA03050.1; -
CC PIR; JQ0096; JQ0096.
CC InterPro; IPR000606; -
CC Pfam; PF01443; Viral_Helicase; 1.
KW ATP-binding; Helicase; RNA replication; RNA-directed RNA polymerase;
KW Transference.
FT NP_BIND 822 829 ATP (POTENTIAL).
FT SEQUENCE 1547 AA; 176320 MW; 6CA4282C6A082622 CRC64;
FT -----
Query Match 52.6%; Score 40; DB 1; Length 1547;
Best Local Similarity 87.5%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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QY 6 YPTKTFPN 13
Db 409 YPTKTFDN 416
|||||
RESULT 13
HMD2_SOLTU STANDARD; PRT; 595 AA.
AC Q41437;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 3-HYDROXY-3-METHYLGUTARYL-COENZYME A REDUCTASE 2 (EC 1.1.1.34) (HMG-
COA REDUCTASE 2) (HMG2.2).
GN HMG2.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. KENNEBEC; TISSUE=Tuber;
RX MEDLINE=97201488; PubMed=9049274;
RA Korth K.L., Sterner B.A., Bhattacharyya M.K., Dixon R.A.;
RT "HMG-CoA reductase gene families that differentially accumulate
transcripts in potato tubers are developmentally expressed in floral
tissues.";
RL Plant Mol. Biol. 33:545-551(1997).
CC -!- FUNCTION: CATALYZES THE SYNTHESIS OF MEVALONATE. THE SPECIFIC
PRECURSOR OF ALL ISOPRENOID COMPOUNDS PRESENT IN PLANTS.
CC -!- CATALYTIC ACTIVITY: (R)-MEVALONATE + COA + 2 NADP(+) -> (S)-3-
HYDROXY-3-METHYLGUTARYL-COA + 2 NADP.
CC -!- PATHWAY: MEVALONATE BIOSYNTHESIS, PLANT ISOPRENOID BIOSYNTHESIS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
RETICULUM.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN YOUNG FLOWERS AND IN MATURE
SEEDS AND OVARIES.
CC -!- SIMILARITY: BELONGS TO THE HMG-COA REDUCTASE FAMILY.
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EMBL; U51985; AAB52551.1; -
DR Mendel; 10574; Soltu;1091;10574.
DR InterPro; IPR002202; -
DR Pfam; PF00368; HMG-CoA_red; 1.
DR PRINTS; PR00071; HMGCOORDTASE.
DR PROSITE; PS00066; HMG_COA_REDUCTASE_1; 1.
DR PROSITE; PS00318; HMG_COA_REDUCTASE_2; 1.
DR PROSITE; PS01192; HMG_COA_REDUCTASE_3; 1.
DR PROSITE; PS01192; HMG_COA_REDUCTASE_4; 1.
DR PROSITE; PS00065; HMG_COA_REDUCTASE_4; 1.
KW Oxidoreductase; Glycoprotein; Endoplasmic reticulum; Transmembrane;
KW Isoprene biosynthesis; NADP; Multigene family.
FT DOMAIN 1 112 MEMBRANE-BOUND (BY SIMILARITY).
FT DOMAIN 113 183 LINKER (BY SIMILARITY).
FT DOMAIN 184 595 CATALYTIC (BY SIMILARITY).
FT TRANSMEM 48 68 POTENTIAL.
FT TRANSMEM 92 112 POTENTIAL.
FT ACT_SITE 278 278 BY SIMILARITY.
FT ACT_SITE 486 486 BY SIMILARITY.
FT ACT_SITE 584 584 GENERAL BASE (BY SIMILARITY).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 342 342 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 455 455 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 588 588 N-LINKED (GLCNAC. .) (POTENTIAL).
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SQ SEQUENCE 595 AA; 63841 MW; 0FA7069849D41D57 CRC64;
Query Match 51.3%; Score 39; DB 1; Length 595;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 RPYVPTKTF 11
:|||||
Db 9 KPVYPSKVF 17
RESULT 14
YCF2_MESVI STANDARD; PRT; 890 AA.
ID YCF2_MESVI
AC Q9MUP8;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 103.9 KDA PROTEIN YCF2 (RF2).
GN YCF2.
OS Mesostigma viride.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
OC Chlorodendrales; Mesostigmataceae; Mesostigma.
OX NCBI_TaxID=41882;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIES-296;
RX MEDLINE=20150907; PubMed=10688199;
RA Lemieux C., Otis C., Turmel M.;
RT "Ancestral chloroplast genome in Mesostigma viride reveals an early
branch of green plant evolution.";
RL Nature 403:649-652(2000).
CC -!- SIMILARITY: BELONGS TO THE YCF2 FAMILY.
-----
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-----
EMBL; AF166114; AAF43852.1; -
DR InterPro; IPR001081; -
DR InterPro; IPR001939; -
DR Pfam; PF00004; AAA; 1.
DR PROSITE; PS00674; AAA; 1.
KW Chloroplast; Hypothetical protein.
SQ SEQUENCE 890 AA; 103935 MW; 43CAEE991AF2C4B CRC64;
```

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Query Match 51.3%; Score 39; DB 1; Length 890;
Best Local Similarity 70.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 RPYVPTKTF 12
:|||||
Db 650 RPYVSVKLF 659
RESULT 15
KINI_YEAST STANDARD; PRT; 1064 AA.
ID KINI_YEAST
AC P13185; Q04606;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PROTEIN KINASE KINI (EC 2.7.1.-).
GN KINI OR YDR122W OR YD9727.17.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
```

```

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCHI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87317589; PubMed=2957690;
RA Levin D.E., Hammond C.I., Ralston R.O., Bishop J.M.;
RT "Two yeast genes that encode unusual protein kinases.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6035-6039(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Murphy L., Shore L., Harris D., Barrell B.G., Rajandream M.A.,
RA Walsh S.V.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN IS PROBABLY A SERINE/THREONINE PROTEIN
CC KINASE.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC NIMI SUBFAMILY.
CC -----
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CC -----
DR EMBL; M69017; AAA34722.1; -
DR EMBL; Z48758; CAN86675.1; -
DR PIR; S42438; S42438.
DR HSSP; Q63450; 1A06.
DR SGD; S0002529; KIN1.
DR InterPro; IPR000719; -
DR InterPro; IPR002290; -
DR Pfam; PF00069; pkinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 120 398 PROTEIN KINASE.
FT NP_BIND 126 134 ATP (BY SIMILARITY).
FT BINDING 149 149 ATP (BY SIMILARITY).
FT ACT_SITE 269 269 BY SIMILARITY.
FT CONFLICT 25 25 S -> R (IN REF. 1).
FT CONFLICT 453 453 T -> H (IN REF. 1).
FT CONFLICT 455 455 V -> G (IN REF. 1).
FT CONFLICT 718 718 A -> R (IN REF. 1).
FT CONFLICT 920 921 NI -> IN (IN REF. 1).
FT CONFLICT 976 976 T -> A (IN REF. 1).
FT CONFLICT 979 980 SI -> T (IN REF. 1).
FT CONFLICT 984 985 KT -> NS (IN REF. 1).
SQ SEQUENCE 1064 AA; 120070 MW; E4104B84A8E45C36 CRC64;

Query Match 51.3%; Score 39; DB 1; Length 1064;
Best Local Similarity 50.0%; Pred.No. 52;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YMRPVYPTKTFP 12
   ||||| 1: :|
Db 802 YMRPMPSSAYP 813

Search completed: July 19, 2001, 14:47:09
Job time: 171 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:46:48 ; Search time 42.51 Seconds
(without alignments)
40.460 Million cell updates/sec

Title: US-09-483-831-69_COPY_201_213
Perfect score: 76
Sequence: 1 YMRPVYPTKTFPN 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_16:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	862	11 Q9R1E6	Q9R1E6 mus musculu
2	76	100.0	863	4 Q13822	Q13822 homo sapien
3	76	100.0	863	4 Q15117	Q15117 homo sapien
4	76	100.0	915	4 Q13827	Q13827 homo sapien
5	70	92.1	885	11 Q64610	Q64610 rattus norv
6	69	90.8	257	11 Q88827	Q88827 rattus norv
7	69	90.8	845	4 Q9NP23	Q9NP23 homo sapien
8	69	90.8	925	4 Q9P1P6	Q9P1P6 homo sapien
9	68	89.5	875	11 P97675	P97675 rattus norv
10	68	89.5	876	11 P70641	P70641 rattus norv
11	65	85.5	875	4 Q14638	Q14638 homo sapien
12	65	85.5	875	11 Q63490	Q63490 rattus norv
13	65	85.5	875	11 P97676	P97676 rattus norv
14	64	84.2	32	6 Q9TRD2	Q9TRD2 bos taurus
15	64	84.2	817	14 Q90761	Q90761 fowlpox vir
16	64	84.2	817	14 Q9J5H1	Q9J5H1 fowlpox vir
17	49	64.5	457	10 Q9SU82	Q9SU82 arabidopsis
18	49	64.5	461	10 Q9SU81	Q9SU81 arabidopsis
19	49	64.5	829	5 P90754	P90754 caenorhabdi

20	48	63.2	479	10 Q9FS13	Q9FS13 spinacia ol
21	48	63.2	496	10 Q9SU83	Q9SU83 arabidopsis
22	47	61.8	479	10 Q42974	Q42974 oryza sativ
23	45	59.2	674	5 P90755	P90755 caenorhabdi
24	43	56.6	173	4 Q9Y5A0	Q9Y5A0 homo sapien
25	43	56.6	343	3 Q9UUN9	Q9UUN9 sporobolom
26	43	56.6	401	4 Q9HAC9	Q9HAC9 mus musculu
27	43	56.6	757	11 Q9WVC8	Q9WVC8 mus musculu
28	42	55.3	429	2 Q69013	Q69013 zymomonas m
29	42	55.3	1004	5 Q9V3H9	Q9V3H9 drosophila
30	41	53.9	247	5 Q44145	Q44145 caenorhabdi
31	41	53.9	381	5 Q9XUV4	Q9XUV4 caenorhabdi
32	41	53.9	427	10 Q43423	Q43423 dianthus ca
33	41	53.9	433	2 Q9PAB9	Q9PAB9 xylella fas
34	41	53.9	453	4 Q9V6X5	Q9V6X5 homo sapien
35	41	53.9	493	10 Q22499	Q22499 zea mays (m
36	41	53.9	1829	5 Q22248	Q22248 caenorhabdi
37	40	52.6	203	13 P79935	P79935 xenopus lae
38	40	52.6	247	10 Q9SN23	Q9SN23 arabidopsis
39	40	52.6	291	10 Q9M4F6	Q9M4F6 brassica na
40	40	52.6	307	5 Q61478	Q61478 dreissena p
41	40	52.6	430	5 Q9NB54	Q9NB54 dreissena p
42	40	52.6	466	10 Q49877	Q49877 lycopersico
43	40	52.6	2066	14 P89920	P89920 oat blue dw
44	40	52.6	3579	5 Q9V5N8	Q9V5N8 drosophila
45	39	51.3	157	5 Q9Y0E8	Q9Y0E8 drosophila

ALIGNMENTS

RESULT 1

Q9R1E6 PRELIMINARY; PRT: 862 AA.

AC Q9R1E6; 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)

DE PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE (EC 3.1.4.1).

GN NP52.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57B/6;

RA Sano K., piao J.-H.;

RT "Cloning and chromosomal assignment of mouse phosphodiesterase

RL I/nucleotide pyrophosphatase (PD-I alpha/autotaxin).";

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF123542; AAD46480.1; -

DR InterPro; IPR001212; -

DR InterPro; IPR002591; -

DR Pfam; PF01033; Somatomedin_B; 2.

DR Pfam; PF01663; Phosphodiester; 1.

DR PRINTS; PR00022; SOMATOMEDIN.

DR PROSITE; PS00524; SOMATOMEDIN_B; 2.

DR SMART; SM00201; SO; 1.

KW Hydrolase.

SQ SEQUENCE. 862 AA; 98918 MW; 641F8F1443E4F8B0 CRC64;

Query Match 100.0%; Score 76; DB 11; Length 862;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
|||||
Db 200 YMRPVYPTKTFPN 212

RESULT 2

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Q13822 ID Q13822 PRELIMINARY; PRT; 863 AA.
AC Q13822;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE AUTOTAXIN-T.
GN ATX-T.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=95074054; PubMed=7982964;
RA Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A.,
RA Sobel M.E., Liotta L.A., Stracke M.L.;
RT "cDNA cloning of the human tumor motility-stimulating protein,
RT autotaxin, reveals a homology with phosphodiesterases.";
RL J. Biol. Chem. 269:30479-30484(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=96158950; PubMed=8579579;
RA Lee H.Y., Murata J., Clair T., Polymereopoulos M.H., Torres R.,
RA Manrow R.E., Liotta L.A., Stracke M.L.;
RT "Cloning, chromosomal localization, and tissue expression of autotaxin
RT from human teratocarcinoma cells.";
RL Biochem. Biophys. Res. Commun. 218:714-719(1996).
DR EMBL; L46720; BAB00855.1; -
DR InterPro; IPR001212; -
DR InterPro; IPR001604; -
DR InterPro; IPR002591; -
DR Pfam; PF01033; Somatomedin_B; 2.
DR PRINTS; PR00022; SOMATOMEDINB.
DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
DR SMART; SM00477; NUC; 1.
SQ SEQUENCE 863 AA; 99017 MW; F960DCE51663BABC CRC64;

Query Match 100.0%; Score 76; DB 4; Length 863;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
Db 201 YMRPVYPTKTFPN 213
|||||

RESULT 3
ID Q15117 PRELIMINARY; PRT; 863 AA.
AC Q15117;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE PHOSPHODIESTERASE I ALPHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96163899; PubMed=8586446;
RA Kawagoe H., Soma O., Goji J., Nishimura N., Narita M., Inazawa J.,
RA Nakamura H., Sano K.;
RT "Molecular cloning and chromosomal assignment of the human brain-type
RT phosphodiesterase I/nucleotide pyrophosphatase gene (PDN2).";
RL Genomics 30:380-384(1995).
DR EMBL; D45421; BAA08260.1; -
DR InterPro; IPR001212; -
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DR EMBL; AF110301; AAF36094.1; JOINED.
 DR EMBL; AF110302; AAF36094.1; JOINED.
 DR EMBL; AF110303; AAF36094.1; JOINED.
 DR InterPro; IPR001212; -.
 DR InterPro; IPR001604; -.
 DR InterPro; IPR002591; -.
 DR Pfam; PF01033; Somatomedin_B; 2.
 DR Pfam; PF01663; Phosphodiesterase 1.
 DR PRINTS; PR00022; SOMATOMEDINB.
 DR PROSITE; PS00524; SOMATOMEDIN_B; 2.
 DR SMART; SM00477; NUC; 1.
 SQ SEQUENCE 925 AA; 104924 MW; 0ECAA063801CAFEB CRC64;

Query Match 90.8%; Score 69; DB 4; Length 925;

Best Local Similarity 100.0%; Pred. No. 0.001; Mismatches 0; Indels 0; Gaps 0;

QY 2 MRPVYPTKTFPN 13
 |||||
 Db 248 MRPVYPTKTFPN 259

RESULT 9
 P97675 PRELIMINARY; PRT; 875 AA.
 AC P97675;

DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE ALKALINE PHOSPHODIESTERASE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 [1]

SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE-97250927; PubMed-9096610;
 RA Scott L.J., Delautier D., Meerson N.R., Trugnan G., Goding J.W., Maurice M.;

RT "Biochemical and molecular identification of distinct forms of alkaline phosphodiesterase I expressed on the apical and basolateral plasma membrane surfaces of rat hepatocytes.";

RL Hepatology 25:995-1002(1997).

DR EMBL; U78787; AAB61535.1; -.

DR InterPro; IPR001212; -.

DR InterPro; IPR001604; -.

DR InterPro; IPR002591; -.

DR Pfam; PF01033; Somatomedin_B; 2.

DR Pfam; PF01663; Phosphodiesterase 1.

DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.

DR SMART; SM00477; NUC; 1.

DR SEQUENCE 875 AA; 99166 MW; 8FEB9A482173D377 CRC64;

Query Match 89.5%; Score 68; DB 11; Length 875;

Best Local Similarity 92.3%; Pred. No. 0.0014; Mismatches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 |||||
 Db 197 YMRPVYPTKTFPN 209

RESULT 10
 P70641 PRELIMINARY; PRT; 876 AA.
 AC P70641;

DT 01-FEB-1997 (TREMBLrel. 02, Created)

DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE PHOSPHODIESTERASE I.

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE=SMALL INTESTINE, PROXIMAL;
 RA Sano K.;
 RT "Molecular cloning of phosphodiesterase I cDNA from rat small intestine";
 RT Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; D30649; BAA06333.1; -.
 DR InterPro; IPR001212; -.
 DR InterPro; IPR001604; -.
 DR InterPro; IPR002591; -.
 DR Pfam; PF01033; Somatomedin_B; 2.
 DR Pfam; PF01663; Phosphodiesterase 1.
 DR PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
 DR SMART; SM00477; NUC; 1.
 SQ SEQUENCE 876 AA; 99328 MW; D2F772C34A0C437A CRC64;

Query Match 89.5%; Score 68; DB 11; Length 876;

Best Local Similarity 92.3%; Pred. No. 0.0014; Mismatches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
 |||||
 Db 197 YMRPVYPTKTFPN 209

RESULT 11

O14638 PRELIMINARY; PRT; 875 AA.

AC O14638;

DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE BETA (EC 3.1.4.1)

DE (PHOSPHODIESTERASE I BETA).

GN PDNFB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

[1]

RN SEQUENCE FROM N.A.

RC TISSUE=PROSTATE;

RX MEDLINE-98008933; PubMed-9344668;

RA Piao J.-H., Goding J.W., Nakamura H., Sano K.;

RT "Molecular cloning and chromosomal localization of PD-Ibeta (PDNFB), a new member of the human phosphodiesterase I genes.";

RL Genomics 45:412-415(1997).

RN SEQUENCE OF 189-875 FROM N.A.

RP Hou S., Wohldmann P., Le T.;

RT "The sequence of Homo sapiens PAC clone DJ0988G15.";

RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

[3]

RN SEQUENCE OF 189-875 FROM N.A.

RA Waterston R.H.;

RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE OF 189-875 FROM N.A.

RP Waterston R.;

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF005632; AAC51813.1; -.

DR EMBL; AC005587; AAD05192.1; -.

DR InterPro; IPR001212; -.

```

DR InterPro: IPR001604; -.
DR InterPro: IPR002591; -.
DR Pfam: PF01033; Somatomedin_B; 2.
DR Pfam: PF01663; Phosphodiesterase_1.
DR PROSITE: PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART: SM00477; NUC; 1.
KW Hydrolase.
SQ SEQUENCE 875 AA; 100096 MW; 329CF41667497BC4 CRC64;

Query Match 85.5%; Score 65; DB 4; Length 875;
Best Local Similarity 84.6%; Pred. No. 0.0048;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
   ||| :|||||||
Db 196 YMRAMYPTKTFPN 208

RESULT 12
Q63490 Q63490 PRELIMINARY; PRT; 875 AA.
AC Q63490;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RB13-5 ANTIGEN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAQUE-DAWLEY; TISSUE-BRAIN;
RX MEDLINE-9524775; PubMed-7730366;
RA Deissler H., Lottspeich F., Rajewsky M.F.;
RT "Affinity purification and cDNA cloning of rat neural differentiation
RT and tumor cell surface antigen gp130RB13-6 reveals relationship to
RT human and murine PC-1."
RL J. Biol. Chem. 270:9849-9855(1995).
DR EMBL: Z47987; CAA88029.1; -.
DR InterPro: IPR001212; -.
DR InterPro: IPR001604; -.
DR InterPro: IPR002591; -.
DR Pfam: PF01033; Somatomedin_B; 2.
DR Pfam: PF01663; Phosphodiesterase_1.
DR PROSITE: PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART: SM00477; NUC; 1.
SQ SEQUENCE 875 AA; 99087 MW; 9BA9FBFBF82DFBA6 CRC64;

Query Match 85.5%; Score 65; DB 11; Length 875;
Best Local Similarity 84.6%; Pred. No. 0.0048;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
   ||| :|||||||
Db 197 YMRAMYPTKTFPN 209

RESULT 13
P97676 P97676 PRELIMINARY; PRT; 875 AA.
AC P97676;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ALKALINE PHOSPHODIESTERASE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE-97250927; PubMed-9096610;
RA Scott L.J., Delautier D., Meerson N.R., Trugnan G., Goding J.W.,
RA Maurice M.;
RT "Biochemical and molecular identification of distinct forms of
RT alkaline phosphodiesterase I expressed on the apical and basolateral
RT plasma membrane surfaces of rat hepatocytes.";
RL Hepatology 25:995-1002(1997).
DR EMBL: U78788; AAB61536.1; -.
DR InterPro: IPR001212; -.
DR InterPro: IPR002591; -.
DR Pfam: PF01033; Somatomedin_B; 2.
DR Pfam: PF01663; Phosphodiesterase_1.
DR PROSITE: PS00524; SOMATOMEDIN_B; UNKNOWN_2.
DR SMART: SM00201; SO; 1.
SQ SEQUENCE 875 AA; 99071 MW; 4205F263E8A933EA CRC64;

Query Match 85.5%; Score 65; DB 11; Length 875;
Best Local Similarity 84.6%; Pred. No. 0.0048;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YMRPVYPTKTFPN 13
   ||| :|||||||
Db 197 YMRAMYPTKTFPN 209

RESULT 14
Q9TRD2 Q9TRD2 PRELIMINARY; PRT; 32 AA.
AC Q9TRD2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 260 KDA MAJOR ACIDIC FIBROBLAST GROWTH FACTOR-STIMULATED
DE PHOSPHOPROTEIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE-94086550; PubMed-7505270;
RA Oda Y., Kuo M.D., Huang S.S., Huang J.S.;
RT "The major acidic fibroblast growth factor (aFGF)-stimulated
RT phosphoprotein from bovine liver plasma membranes has aFGF-stimulated
RT kinase, autophosphorylation, and alkaline nucleotide phosphodiesterase
RT activities.";
RL J. Biol. Chem. 268:27318-27326(1993).
SQ SEQUENCE 32 AA; 3699 MW; 5CCFFA9EB5E6927 CRC64;

Query Match 84.2%; Score 64; DB 6; Length 32;
Best Local Similarity 91.7%; Pred. No. 0.0002;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MRPVYPTKTFPN 13
   ||||| |||
Db 2 MRPVYPTKTFPN 13

RESULT 15
Q90761 Q90761 PRELIMINARY; PRT; 817 AA.
AC Q90761;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ALKALINE PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-
DE NUCLEOTIDE PHOSPHODIESTERASE).
GN PCL
OS Fowlpox virus.

```

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OX Avipoxvirus.
RN NCBI_TaxID=10261;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP-9;
RX MEDLINE=98325194; PubMed=9658122;
RA Laidlaw S.M., Anwar M.A., Thomas W., Green P., Shaw K., Skinner M.A.;
RT "Fowlpox virus encodes nonessential homologs of cellular alpha-SNAP,
PC-1, and an orphan human homolog of a secreted nematode protein.";
RL J. Virol. 72:6742-6751(1998).
CC -|- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
OLIGO-NUCLEOTIDES.
CC EMBL; AJ006408; CAA07014.1; -.
DR InterPro: IPR001604; -.
DR InterPro: IPR002591; -.
DR Pfam: PF01663; Phosphodiester; 1.
DR SMART; SM00477; NUC; 1.
KW Hydrolase.
SQ SEQUENCE 817 AA; 94004 MW; CB68DA0508CC568E CRC64;

Query Match 84.2%; Score 64; DB 14; Length 817;
Best Local Similarity 91.7%; Pred. No. 0.0066;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 MRPVYPTKTFPN 13
Db 155 MRPVYPTNTEPN 166
|||||

Search completed: July 19, 2001, 14:46:49
Job time: 172 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 14:41:32 ; Search time 34.65 seconds
(without alignments)
1600.893 Million cell updates/sec

Title: US-09-483-831-69
Perfect score: 5019
Sequence: 1 MARRSFQSQIISLTFV.....RSYPEILTKYLTHTYSEI 915

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5019	100.0	915	17	AAR86596
2	5019	100.0	915	22	AA1987
3	4681	93.3	863	22	AA1988
4	4632	92.3	859	22	AA1991
5	4533	90.3	829	17	AAR86578
6	4430.5	88.3	858	22	AA1997
7	4430.5	88.3	858	22	AA1999
8	4429.5	88.3	858	22	AA1998
9	4426.5	88.2	858	22	AA1986
10	4423.5	88.1	858	22	AA1995
11	4422.5	88.1	858	22	AA1995

12	4341	86.5	849	17	AAR86595
13	4306	85.8	885	22	AA1989
14	4279	85.3	979	17	AAR86580
15	3842	76.5	788	17	AAR86579
16	1955.5	39.0	873	21	AA198620
17	1955.5	39.0	925	16	AA198620
18	1955.5	39.0	925	20	AA198620
19	1955.5	39.0	925	21	AA198620
20	1954.5	38.9	873	21	AA198621
21	646.5	12.9	457	21	AA198621
22	609	12.1	461	21	AA198621
23	609	12.1	465	21	AA198621
24	599	11.9	400	21	AA198621
25	569	11.3	359	21	AA198621
26	512	10.2	453	20	AA198621
27	512	10.2	453	20	AA198621
28	512	10.2	453	22	AA198621
29	484	9.6	338	21	AA198621
30	467	9.3	440	21	AA198621
31	465.5	9.3	477	21	AA198621
32	465.5	9.3	477	21	AA198621
33	465.5	9.3	477	22	AA198621
34	465	9.3	411	20	AA198621
35	465	9.3	428	20	AA198621
36	360	7.2	438	21	AA198621
37	357	7.1	355	19	AA198621
38	357	7.1	355	20	AA198621
39	241.5	4.8	133	21	AA198621
40	200	4.0	92	21	AA198621
41	179	3.6	109	19	AA198621
42	141	2.8	39	21	AA198621
43	134	2.7	111	13	AA198621
44	134	2.7	182	12	AA198621
45	134	2.7	452	16	AA198621

ALIGNMENTS

RESULT 1
AAR86596
ID AAR86596 standard; Protein; 915 AA.

AC AAR86596:
DT 01-JUL-1996 (first entry)
DE A2058 autotaxin protein.

KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
XX melanoma cell; tumour; antibody; cancer diagnosis; therapy.

OS Homo sapiens.
PN WC9532221-A2.
PD 30-NOV-1995.
PF 24-MAY-1995; 95WO-US066613.
PR 28-NOV-1994; 94US-0346455.
PR 25-MAY-1994; 94US-0249182.

(USSS) US DEPT HEALTH & HUMAN SERVICES.

Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;

WPI; 1996-020533/02.

Autotaxin motility stimulating protein, and DNA encoding it - used
in cancer diagnosis and therapy

Claim 4; Page 91-94; 112pp; English.

bad data

CC Transgenic animals that overexpress autotaxin are models for
XX human metabolic diseases.

SQ Sequence 915 AA;

Query Match 100.0%; Score 5019; DB 22; Length 915;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRSFQSCQIISLFFAVGVSICLGTAFHRIKRAEGWEGPPVVLSDSPWNTNIGSGCK 60
DB 1 marrrsfqscqilslffavgsiclgftahrikraegweegpptvlssdpwninsgsk 60
QY 61 GRCELEQAGPPDCRDNLCYSKSCCHDFELCLTKTARGWECTKDRGCEVNEENACHC 120
DB 61 grcfelqagppdcrcdnlcyskscchdfelcltkargwectkdrcevevneenachc 120
QY 121 SEDCLARGDCCTNYQVVCYKGSHEWVDDCEETKAECPAGFVRPPLIIIFSVDFRASYMK 180
DB 121 sedclargdcctnygvvcykgshewvddceetkaecpagfvrppliiifsvdgrasymk 180
QY 181 KGSVMENIEKLRSCGTHSPMRVPYPTKTPNLYTLATGLYPESHGIVGNSMYDPVEDA 240
DB 181 kgsvmenieklrscgthspmrpyptktpnlytlatglypeshgvgnsmypdvda 240
QY 241 TFLHGRKFNHRWNGGLOPLWITATKQGVKAGTFWVSVIPHERILATLRLWLTLPDHER 300
DB 241 tflhgrkfnhrwnggloplwitatkqgvkagtfwsvvipherilatlrlwltlpdher 300
QY 301 PSVYAFYSEQPDFSGHKYKPGFPBESSYSGFTPAKRKRKVPAPKRRQRPVAPPKRRR 360
DB 301 psyafysepdfsgkypgfpbessygsftpakrkrkvapkrqrpvapppkrrr 360
QY 361 KIHMDHYAAETRODKMTNPLREIDKIVGQMDGLKQLKRRCVNVIIFVGDHGMEDVTC 420
DB 361 kihmdhyaaetrqdkmntplreidkivgqmdglkqlkrrcvnvifvgdhgmedvtcd 420
QY 421 RTEFLSNLYNVDDITLVPGTLGRIRSKFSNNAKVDPKAITANLTCKRPDQHFKPYLKQH 480
DB 421 rteflsnlynvdditlvpgtlgrirskfsnnakvdpkaiitanltckrpdqhfkyplkqh 480
QY 481 LPKRLHYANNRRIEDIHLLVRRWHVARKPLDVYKPSGKCFEQGDHGFQDNKVNMQWVF 540
DB 481 lpkrlhyannrriedihllvrrwhvarkpldvkykpsgkcfegqdhgfdnkvnsmqwtvf 540
QY 541 VGYGPTFKYTKVPPFENIELYNVCMDDLGLKPAFNNNGTHGSLNHLRTNFRPTMPPEV 600
DB 541 vgygptfkytkvppfenielynvcmddlglkpaafnnngthgslnhlrrtnfrptmpeev 600
QY 601 TRNYPGIMYLOSDFDGLCTODDKVEPKNKLDELNKLRLHTKGSTEERHLLYGRPAVLRT 660
DB 601 trnypgimylsdfdgldctoddkvepknkldeknklrlhtkgsteerhlllygrpavlyrt 660
QY 661 RYDLYHTDESGYSEFLMLLWTSYVSKOAEVSSVPDHLTSCVRPDRVRSFSONCL 720
DB 661 rydlyhtdesgyseflmlwtsyvskaevssvpdhltsctvrpdrvrspfsqnc 720
QY 721 AYKNDKQMSYGFLEPPYLSSSPEAKYDAFLVTNMVPMYPAFRKRVNMYQFQRLVKKYASER 780
DB 721 aykndkmsygfleppylssspeakydafvltnmvpmypafkrvnmvmyqfqrllvkkya 780
QY 781 NGNVISGPIFYDYDGLHDPEDKIKQVEGSSIPVPTHYSIITSCLDFTQPADKCDGP 840
DB 781 ngnvisgpifydydglhdpedkikqvegssipvpthysiltsclfdtqpdkcdgp 840
QY 841 LSVSFFLPHRPDNEECNSSEDESKWVEELMKMHTARVROIEHLTSLDFPRKTSRSTPE 900
DB 841 lsvsfflphrpndeeecnsedeskvwveelmkmtarvrroiehltsldfprktsrype 900
QY 901 ILTKYTLHTYSEI 915
DB 901 iltktylhtysei 915

RESULT 3

AA71988
ID AAY71988 standard; Protein; 863 AA.

XX
AC AAY71988;

XX
DT 28-MAR-2001 (first entry)

XX
DE Human teratocarcinoma autotaxin.

XX
KW Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
type I phosphodiesterase activity; ATP pyrophosphatase activity;
ATPase; adenosine-5'-triphosphatase activity; teratocarcinoma.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers

FT Binding-site 127..129
FT /label= RGD_binding_domain

FT Active-site 201..213
FT /note= "Autotaxin phosphodiesterase catalytic site"

XX
PN WO200068386-A1.

XX
PD 16-NOV-2000.

XX
PF 05-MAY-2000; 2000WO-US12402.

XX
PR 07-MAY-1999; 99US-0306979.

XX
PA (ZYMO) ZYMOGENETICS INC.

XX
PI Kelly JD;

XX
DR WPI; 2001-007397/01.

XX
PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
obesity, stimulate glucose uptake by cells and inhibit lipolysis -
Claim 27; Page 108-110; 126pp; English.

XX
CC The present sequence is autotaxin isolated from human
teratocarcinoma cells. Autotaxin is a glycoprotein cytokine which
increases insulin signalling in adipose tissue by producing substrate
for adenosine receptors, resulting in inhibition of lipolysis,
decreased hepatic gluconeogenesis and serum glucose levels, and
increased insulin sensitivity. It also inhibits differentiation
of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-
triphosphatase (ATPase) and ATP pyrophosphatase activities.
Autotaxin and its analogues are used to stimulate glucose uptake
by cells, particularly to reduce serum glucose levels for
treatment of non-insulin dependent diabetes (NIDDM) in humans,
or generally any condition associated with elevated serum levels
of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
Transgenic animals that overexpress autotaxin are models for
human metabolic diseases.

XX
SQ Sequence 863 AA;

Query Match 93.3%; Score 4681; DB 22; Length 863;
Best Local Similarity 93.8%; Pred. No. 0;

Matches 858; Conservative 2; Mismatches 3; Indels 52; Gaps 1;

QY 1 MARRSFQSCQIISLFFAVGVSICLGTAFHRIKRAEGWEGPPVVLSDSPWNTNIGSGCK 60

DB 1 marrrsfqscqilslffavgsiclgftahrikraegweegpptvlssdpwninsgsk 60

QY 61 GRCFELQAGPPDCRNDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGVRNEENACHC 120
|||||
Db 61 grcfelqagppdcrcndnlcksytsccchdfdelclktarawectkdrcevrneenachc 120
QY 121 SEDCLARGCCCTNYQVCKGESHWDDECEIEKAAECFAGFVRPPLIIFSVGDFRASYMK 180
|||||
Db 121 sedclargccctnyqvckgeshwddceekaaecpagfvrppliifsvdgrasymk 180
QY 181 KGSKVMPTNEKLRSCGTHSPYMRPVPTKFPNLTYLATGLYPESHGIVGNSMYDVPFDA 240
|||||
Db 181 kgskvmptneklrscgthspymrpvptkfpnltylatglypeshgvnsmydvpfda 240
QY 241 TFLHREKFNHRWGGQPLWITATKQGVKAGTFEFSWIPHERRIILTLRWLTLPDHER 300
|||||
Db 241 tflhrgrefnhrwggqplwitatkgvkgagtfefswipherrililtlrlwltlpdher 300
QY 301 PSVYAFYSQOPFSGHKYGFPGFEESYSGFPTPAKRPKRKVPAPKRRPPVAPPKRRR 360
|||||
Db 301 psvyafysepfsgkhkgfpgfeesysgfpptpakrpkrvpaprpkrrppvapkrrr 360
QY 361 KIHRMDHYAAETQDKWTPLEIDKIVGOLMDGLKOLKLRRCVNVIFVGDHGMEDVTC 420
|||||
Db 361 kihrmdhyaaetqdkwtpleidkivgolgmdglkolkrrcvnvifvgdhgmmedvtd 420
QY 421 RTEFLSNLYTNVDITLPGTLGRIRSKFENNAYDKPAAIANLTCKRPQDQHFYPLKQH 480
|||||
Db 421 rteflsnlytnvdiitlpgtlgrirskfennaydkpaaianltckrpqdhfypylkqh 480
QY 481 LPKRLHYANNRRITIEDHLVERHWARKPLDVYKPSGKCFPGDGHGDFGNKNSMOTVF 540
|||||
Db 481 lpkrlhyannrritiedhlverhwarkpldvypskgkcfpgdghgdfgnknsmtotvf 540
QY 541 VGVGPTFKYTKYPPFENTELYNMCDLLGLKPAPNGTHGSLNHLRTNFTPTMPEEV 600
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Db 541 vgvgptfkytkyppfentelynmcdllglkpapngthgslnhlrtntftptmpeev 600
QY 601 TRPNYGMVQLQSDFDLGCDCDKVPEKNLDELNLKRLHTKGSTEERHLYGRPAVLYRT 660
|||||
Db 601 trpnygmvlqsdfdlgcddkvpknldelnkrlhtkgsteerhlygrpavlyrt 660
QY 661 RYDILYHTPESYSEIFMLLWTSYTVSKOAEVSSVPDHLTSCVRPDVVRVSPFSQNC 720
|||||
Db 661 rydilyhtpesyseifmlwtsytsvskoaevsyvpdhltscvrpdvvrspfsqnc 720
QY 721 AYKNDQMSYGFLLPFPYLLSSPPEAKYDAFLVTNMVMPYPAKRVNWFQRLVVKYASER 780
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Db 721 aykndqmsygfllpfpylssppeakydafvtnmvmpyapkrvwnwfqrlvvykaser 780
QY 781 NGVNVISGPIFDYDGLHDFEDKIKOYVEGSSIPVPTHYYSITSLDFTQADKCDGP 840
|||||
Db 781 ngvnvisgpifdydgldhdfedkikoylegssipvpthyysitlsldftqadkcdgp 840
QY 841 LSVSSFILPHRPNDEESCNSESKWVEELMKHMTARVDRDIEHLTSLDFPRKTSRSYPE 900
|||||
Db 841 lsvssfilphrpdneescnseskwveelmkhmtarvdrdiehltsldfprktsrsype 900
QY 901 ILTKYLYHTYSEI 915
|||||
Db 849 iltkylhtysei 863

RESULT 4

AAV71991
ID AAY71991 standard; Protein; 859 AA.
XX
AC AAY71991;
XX
DT 28-MAR-2001 (first entry)
XX
DE Human autotaxin protein.
KW Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;

KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Domain 8..26
FT /note= "Putative transmembrane domain"
FT Cleavage-site 44..45
FT Binding-site 123..125
FT /label= RGD_binding_domain
FT Active-site 197..209
FT /note= "Putative phosphodiesterase active site"
XX WO200068386-A1.
XX 16-NOV-2000.
XX 05-MAY-2000; 2000WO-US12402.
XX 07-MAY-1999; 99US-0306979.
XX (ZYMO) ZYMOGENETICS INC.
XX Kelly JD;
XX WPI; 2001-007397/01.
XX N-PSDB; AAD02133.
XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and
XX obesity, stimulate glucose uptake by cells and inhibit lipolysis -
XX Claim 27; Page 119-121; 126pp; English.
XX The present sequence is human autotaxin protein.
XX Autotaxin is a glycoprotein cytokine which increases
XX insulin signalling in adipose tissue by producing substrate for
XX adenosine receptors, resulting in inhibition of lipolysis,
XX decreased hepatic gluconeogenesis and serum glucose levels, and
XX increased insulin sensitivity. It also inhibits differentiation
XX of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-
XX triphosphatase (ATPase) and ATP pyrophosphatase activities.
XX Autotaxin and its analogues are used to stimulate glucose uptake
XX by cells, particularly to reduce serum glucose levels for
XX treatment of non-insulin dependent diabetes (NIDDM) in humans,
XX or generally any condition associated with elevated serum levels
XX of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
XX Transgenic animals that overexpress autotaxin are models for
XX human metabolic diseases.
XX Sequence 859 AA;

Query Match 92.3%; Score 4632; DB 22; Length 859;
Best Local Similarity 93.7%; Pred No. 0;
Matches 848; Conservative 3; Mismatches 2; Indels 52; Gaps 1;
QY 11 QIISLTFAGVYSICLGFTAHRIKRAEGWEGPPTVLSDPWTNISGCKGRCFELQEAG 70
|||||
Db 7 riisiftavgvniclgtfahrikraegwdegpptvlsdpwtinsgckgrcfelqag 66
QY 71 PPDRCNDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGVRNEENACHCEDCLARGDC 130
|||||
Db 67 ppdrcndnlcksytsccchdfdelclktargwectkdrcevrneenachsedclargdc 126
QY 131 CTNYQVCKGESHWDDECEIEKAAECFAGFVRPPLIIFSVGDFRASYMKSKVMPNIE 190
|||||
Db 127 ctnyqvckgeshwddceekaaecpagfvrppliifsvdgrasymksgkvmnpnie 186
QY 191 KLRSCGTHSPYMRPVPTKFPNLTYLATGLYPESHGIVGNSMYDVPFATFLHREKFX 250
|||||

Db 187 klrscgthspyrpvyptktfplnylatglypeshgivgnsmypdvfdatfhlrgrekf 246
QY 251 NHRWGGQPLWITATOGVKAGTFFNSVIPHERRIITILRWLTLPDHERSVAFYSEQ 310
Db 247 nhrwggqplwitatkqgkvagtfvsvipherritliqwtlclpdpshersvafyseq 306
QY 311 PPSGHKYGPFPGFEESYSGPFTPAKRPRKRVAPKRQERPVAPPKRRRKIRHMDHYAA 370
Db 307 pdfsgkhygpfge----- 320
QY 371 ETRQDKMTNPLREIDKIVGQMDGLKQKLRRCVNVIFVGDHGMEDVTCRTEFLSNYLT 430
Db 321 -----mtnplreidklvgldgkqlkhrvcnvifvgdhgmedvctdrteflsnlyt 374
QY 431 NVDDITLVPGTIGRIRSKFSNNAKYDPKAIANLTCKPQDHFYKQLHLPKRLHANN 490
Db 375 nvddilvpgtigrirskfsnnakydpkaiantckpdkqgfkpylkqhlprlhyann 434
QY 491 RRIEDTHLLVERHWHVARKPLDYKYPSPGKCFQGDHGFONKVNMSQTVFVGYPGTFKYK 550
Db 435 rriedthllverwhvarkpldykypsgkcfqgdhgfndkvnsmqtvfvgypgtfkyk 494
QY 551 TKVPPENIELYNMCDLLGLKAPNNGTHGSLNHLRTNTFRTPMPEEVRPNYPGIMY 610
Db 495 tkvppfenielynvmcdllglkpaungthgslnhlrtntfrtpmpeevtrpnypgimy 554
QY 611 LQSDFDLCTCDDKVEPKNKLDELNKLHRTKSTEEHLLYGRPAVLYRTRDYLYHTDF 670
Db 555 lqsdfdlctcddkvepknldeinrlhrtkgateerhllgrpavlyrtrdylyhtdf 614
QY 671 ESYGSEIFLMLLWTSVTSKQAEVSSVPDHLTSCVRPDVRVSPFSQNLAYKNDKQMSY 730
Db 615 esygseiflmlwtstvtskqaevssvpdhltscvrpdvrsvpsfsgnclaykndkmsy 674
QY 731 GFLPPYLSPPSPAKYDAFLVTNMVMPYAFKRWNYFQRLVKKYASERGNVNVISGPI 790
Db 675 gflfpylsspspeakydaflvtnmvmpyafkrwnyfqrlvkkysaserngvnvisgpi 734
QY 791 FDYDGLDHTDEKIKQYVEGSSIPVPTHYYSITSCLDFTQPADKCDGGLSVSSFILPH 850
Db 735 fdydgldhtedkikqyvegssipvpthyysitscldftqpadkcdgplsvssfilph 794
QY 851 RPDNESSCNSSDESKWVEELMKWHARVDRDIEHLTSLDFPRKTSRYPETLLTKTYLHT 910
Db 795 rpdnecssnssedeskwveelmkwharvdrdienhltsldfprktsrypeitlktlyht 854
QY 911 YESEI 915
Db 855 yesei 859
RESULT 5
AAR86578
ID AAR86578 standard; Protein; 829 AA.
AC AAR86578;
XX
XX
XX 28-JUN-1996 (first entry)
DT
XX Autotaxin derived from melanoma cell line A2058.
DE
XX Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMP;
KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.
XX
XX Homo sapiens.
OS
XX
XX WO9532221-A2.
PN
XX
XX 30-NOV-1995.
PD
XX
XX 24-MAY-1995; 95WO-US06613.
PF
XX
XX 28-NOV-1994; 94US-0346455.
PR

PR 25-MAY-1994; 94US-0249182.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;
XX WPI; 1996-020533/02.
XX N-PSDB: TO6612.
DR
XX Autotaxin motility stimulating protein, and DNA encoding it - used
PT in cancer diagnosis and therapy
XX
XX Claim 4; Page 57-60; 112pp; English.
XX
CC AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is
CC an autocrine motility stimulating protein which is present in cancer
CC cells. ATX stimulates both random and directed migration of melanoma
CC cells. The tumorous form of ATX is a secreted protein, while the
CC transmembrane bound form is not present in tumour cells. The cDNA
CC encoding this sequence can be used in a vector, to transform cells. The
CC recombinant cells can then be used to produce the peptide sequences.
CC Antibodies specific for these sequences can be produced, and can be used
CC in cancer diagnosis and therapy. Different sites of localisation of the
CC protein are utilised for diagnosis and prognosis of the stages of tumour
CC progression. The sequences can be used in treatment methods to
CC advantageously block the activity of the secreted form of ATX, while
CC having little effect on the membrane form of ATX.
XX
SQ Sequence 829 AA;
Query Match 90.3%; Score 4533; DB 17; Length 829;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 87 CHDFDELCLKTARGWECTKDRGGEVRNEENACHCEDCLARGDCTNYOVVCKGESHWVD 146
Db 1 chdfdelclktargwectkdrgevrneenachcedclargdctnyovvckgeshwvd 50
QY 147 DCEBIKAEACPAQVRPPLIIFSVDFRASYMKKSGKVMPIEKLRSCTGTHSPYMRPY 206
Db 61 ddceebikaepaqvrrpplliifsvdfgrasyymkksgkvmvpnieklrscgthspymrpy 120
QY 207 PTKFPNLYTLATGLYPESHGIVGNSMYDPVDFATFHLRGREKFNHRWGGQPLWITATK 266
Db 121 ptktfpnyltlatglypeshgivgnsmypdvfdatfhlrgrekfnhrwggqplwitatk 180
QY 267 QGVKAGTFFWSVVIPIHERRIITILRWLTLPDHERSVVAFYSEQPDFSGHKYGPFGPEES 326
Db 181 qgvkagtffwsvvipherritliilrwltlpdherpsvafyseqpdfsgkhygpfgepes 240
QY 327 SYGSPFTPAKRPRKRVAPKRQERPVAPPKRRRKIRHMDHYAAETRQDKMTNPLREIDK 386
Db 241 sygspftpakrprkrvapkrrqerpvapppkrrrkirhmdhyaaetrqdkmntplreidk 300
QY 387 IVGQLMDGLKQLRRCVNVIFVGDHGMEDVTCRTEFLSNYLTWVDDITLVPGTLGRIR 446
Db 301 ivgqlmdgkqlkrrcvnvifvgdhgmedvctdrteflsnlyltvdditlvpgtlgrir 360
QY 447 SKFSNNAKYDPKAIANLTCKPQDHFYKQLHLPKRLHYANNRIEDTHLLVERHWHV 506
Db 351 skfsnnakydpkaiantckpdkqgfkpylkqhlprlhyannriedthllverwhv 420
QY 507 ARKPLDYVKKPSGKCFQGDHGFONKVNMSQTVFVGYPGTFKYKTKVPPENIELYNVNC 566
Db 421 arkpldyvkpsgkcfqgdhgfndkvnsmqtvfvgypgtfkyktkvpfenielynvmc 480
QY 567 DLLGLKAPNNGTHGSLNHLRTNTFRTPMPEEVRPNYPGIMY LQSDFDLCTCDDKVE 626
Db 481 dllglkpaungthgslnhlrtntfrtpmpeevtrpnypgimy lqsdldlctcddkve 540
QY 627 PKNKLDENKLHRTKSTEEHLLYGRPAVLYRTRDYLYHTDFESGYSIEIFLMLLWTSY 686
PR

Db 541 pknkideinkrlhtkgsteerhlygrpavlyrtrydilyhtdfesgyseifmlllwtsty 600
 Qy 687 TVSKQAEVSSVPDHLTSCVRPDRVSPFSQNCLAYKNDKQMSYGLFFPYLSSPEAKY 746
 Db 601 tsvkqaeavssvpdhltsctvrpdrvspsqncalaykndkqmsyglffpylsspeaky 660
 Qy 747 DAFLYTNMVPMPYPAKRWVNYFORVLVKYASERNGVNWSGPIFYDYDGLDHTDEKIK 806
 Db 661 daflvtmvmvmpyafkrvwnyqfgrvlvkkysaerngvnvisgpifydydglhdtedkik 720
 Qy 807 QVGESSIPVPHYYSIIITSCLDFTQPADKCDGPLSVSSFIPLPHRPDNEESCNSSEDESK 866
 Db 721 qvgeavssipvphhyysiiitscldfcqpadkcdgplsvsffilphrpndneescnsedesk 780
 Qy 867 WYEEELMKHMTARVDRDIEHLTSLDFRKTGRSYPEILTLKTYLHTYSEI 915
 Db 781 wyeelmkmhtarvdrdiehltsldfrktrsypeliltktylhtysei 829

RESULT 6
 AAY71997
 ID AAY71997 standard; Protein; 858 AA.
 AC AAY71997;
 XX
 DT 28-MAR-2001 (first entry)
 XX
 DE Rat autotaxin variant (S236T).
 XX
 KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
 KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
 KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
 KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
 KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
 KW ATPase; adenosine 5'-triphosphatase activity; mutant; mutein; variant.
 XX
 OS Rattus sp.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 236
 FT /note= "Wild type Ser substituted by Thr"
 FT
 XX
 PN WO200068386-A1.
 XX
 XX PD 16-NOV-2000.
 XX
 XX PF 05-MAY-2000; 2000WO-US12402.
 XX
 XX PR 07-MAY-1999; 99US-0306979.
 XX
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX
 XX PI Kelly JD;
 XX
 XX DR WPI; 2001-007397/01.
 XX
 XX PT New autotaxin proteins, useful e.g. for treating diabetes mellitus and
 XX obesity, stimulate glucose uptake by cells and inhibit lipolysis -
 XX
 XX PS Disclosure; Page -: 126pp; English.
 XX
 XX The present sequence is variant (S236T) of rat autotaxin protein.
 XX Autotaxin is a glycoprotein cytokine which increases insulin
 XX signalling in adipose tissue by producing substrate for adenosine
 XX receptors, resulting in inhibition of lipolysis, decreased hepatic
 XX gluconeogenesis and serum glucose levels, and increased insulin
 XX sensitivity. It also inhibits differentiation of adipocytes.
 XX Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
 XX (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
 XX analogues are used to stimulate glucose uptake by cells, particularly
 XX to reduce serum glucose levels for treatment of non-insulin dependent
 XX diabetes (NIDDM) in humans, or generally any condition associated

CC with elevated serum levels of glucose, lipid or free fatty acid
 CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
 CC autotaxin are models for human metabolic diseases.
 CC Note: The present sequence is not shown in the specification
 CC but is derived from rat autotaxin protein sequence found in
 CC page 101-104 of sequence listing (RAY71986).
 XX Sequence 858 AA;
 SQ

Query Match 88.3%; Score 4430.5; DB 22; Length 858;
 Best Local Similarity 88.7%; Pred. No. 0;
 Matches 803; Conservative 30; Mismatches 19; Indels 53; Gaps 2;

QY 11 QIISLFTFAVGVSTICLGFTAHRIKRAEGWEGPPTVLSDSPWTNISGKRCGFELQAG 70
 Db 7 rvslftfaivgvsticlgftasrkrae-wdegpptvlstdspwtntsgskgrcfelqevg 65
 QY 71 PPDCRDNLCSTYSCCHDFDELCLKTARGWECTKDCGEVNRNEENACHCEDCLARGDC 130
 Db 66 pdcrcdnlcsystscchdfdelclktargwectkdcgevrneenachcedclargdc 125
 QY 131 CTNYQVVCKGESHWDDDCBEIKAAECPAGFVRPPLIIFSVGDFRASYMKSGKVMNIE 190
 Db 126 ctnyqvckgeshwddcceikvpecpagfvrpplliifsvdgfrasymksgkvmnie 185
 QY 191 KLRSCGTHSPYMRPVYPTKTPNLYTLATGLYPESHGIVGNSMYDPVDFATFHLRGREKF 250
 Db 186 klrscgthspymrpvypktfnpnlytlatglypeshgivgnsmydvpdfatfhlrgrekf 245
 QY 251 NHRWGGQPLMITATKQGVKAGTEFFWSVIPHERRIITLRLWTLDPHERPSVYAFYSEQ 310
 Db 246 nhrwggqplmitatkqgvragtffwsvipherriitlqlwslpdrnpsvyafyseq 305
 QY 311 PDPSGHYKGFPGPESSYSGSPTTAKRKPVKAPKRQRPVAPPKRRKRRIHRMDHYAA 370
 Db 306 pdfsgghkygpfge----- 319
 QY 371 ETRQDKMTNPLREIDKIVGQLMDGLKOLKLRRCVNVIVFGDHGMEDVTCDRTEFLSNVLT 430
 Db 320 -----mtnplreidktvgqlmdglkqlrhrcvnnvifvgdhgmedvtcdrtelfsnvlt 373
 QY 431 NVDDITLVPGTGLGRIRKFSNNAKYDKAIITANITCKKPDQHKPKYLOKHLPKRLHYANN 490
 Db 374 nvdditlvpgtglgraksnnskydkptianitckkpdqhkpkymkqhlprkrlhyann 433
 QY 491 RRIEDIHLVERHWVARKPLDVKYKSGCKFFOGDGHGFKNVNSMQTVFVGYPTRKYK 550
 Db 434 rriedihllvdrwhvarkpldvkykpsgckffgghgfdnkvnsmqtvfvgyptrkyr 493
 QY 551 TKVPPFENIELYNVCMCDLGLKPPAPNNGTHGSLNHLRLTNTFRPTMPEEVRPNYPGIMY 610
 Db 494 tkvppfenielynvmcdllglkppapnngthgslnhlrltntrfrcpmpdevsrpnypgimy 553
 QY 611 LQSDFDLGCCTCDKVEPKNLDELNKLHKTGSTEEHLLYGRPAVLYRTRYDLYHTDF 670
 Db 554 lqsefdlgtctcdkvepknlleelnklhckgsteehllgrpavlyrtrydlyhtdf 613
 QY 671 ESGYSEIFMLLWTSYTVSKQAEVSSVPDHLTSCVRPDRVSPFSQNCLAYKNDKQMSY 730
 Db 614 esgyseifmlplwtsytiskqaeavssipehltnrcvrpdrvspsqncalaykndkqmsy 673
 QY 731 GFIFPPYLSSSPEAKYDAFLVTNNVMPYPAKRWVNYFORVLVKYASERNGVNWSGPI 790
 Db 674 gfifppyllsspeakydaflvtmvmvmpyafkrvwnyqfgrvlvkkysaerngvnvisgpi 733
 QY 791 FDYDYGDLHDEDEKIKQYVGESSIPVPHYYSIIITSCLDFTQPADKCDGPLSVSSFIPLH 850
 Db 734 fdynydgldrdeideikyvgeavssipvphhyysiiitscldftqpadkcdgplsvsffilph 793
 QY 851 RPNEESCNSSEDESKWEEELMKHMTARVDRDIEHLTSLDFRKTGRSYPEILTLKTYLHT 910
 Db 794 rpdndescnsdeskswyeelmkmhtarvdrdiehltsldfrktrsypeliltktylht 853

XX DE Rat autotaxin variant (R265K).

XX KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;

XX KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;

XX KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;

XX KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;

XX KW type I phosphodiesterase activity; ATP pyrophosphatase activity;

XX KW ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.

XX OS Rattus sp.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 265

XX FT /note= "Wild type Arg substituted by Lys"

XX WO200068386-A1.

XX PN 16-NOV-2000.

XX PD 05-MAY-2000; 2000WO-US12402.

XX PF 07-MAY-1999; 99US-0306979.

XX PR (ZYMO) ZYMOGENETICS INC.

XX PA Kelly JD;

XX PI WPI; 2001-007397/01.

XX DR New autotaxin proteins, useful e.g. for treating diabetes mellitus and

XX PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -

XX PT Disclosure; Page -: 126pp; English.

XX PS The present sequence is variant (R265K) of rat autotaxin protein.

XX CC Autotaxin is a glycoprotein cytokine which increases insulin

CC signalling in adipose tissue by producing substrate for adenosine

CC receptors, resulting in inhibition of lipolysis, decreased hepatic

CC gluconeogenesis and serum glucose levels, and increased insulin

CC sensitivity. It also inhibits differentiation of adipocytes.

CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase

CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its

CC analogues are used to stimulate glucose uptake by cells, particularly

CC to reduce serum glucose levels for treatment of non-insulin dependent

CC diabetes (NIDDM) in humans, or generally any condition associated

CC with elevated serum levels of glucose, lipid or free fatty acid

CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress

CC autotaxin are models for human metabolic diseases.

CC Note: The present sequence is not shown in the specification

CC but is derived from rat autotaxin protein sequence found in

CC page 101-104 of sequence listing (AAY71986).

XX XX

SQ Sequence 858 AA;

Query Match 88.38; Score 4429.5; DB 22; Length 858;

Best Local Similarity 88.78; Pred. No. 0;

Matches 803; Conservative 30; Mismatches 19; Indels 53; Gaps 2;

QY 11 QIISLFTFAVGVSICLGTAFHRAEGWECPPTVLSDSPTNTSGCKGRCFELQEG 70

Db 7 rvisiffafsvnclgtfbsrikrae-wdegppcvlsdpswntsgckgrcfelqevg 65

QY 71 PPDCRCNLCYSYSCCHDFDELCLKTARGWECKTDRGCEVNEENACHSCSDCLARGDC 130

Db 66 ppdcrcnclksyscchdfclclktargwecktdrgcevrneenachscsdclsrqdc 125

QY 131 CTNTQVCKGSHWVDDCEIEKAECAGFVRPPLIFSDGFRASYMKGSKVMPNIE 190

Db 126 ctnygvckgshwvddcceikvpcpagfvrpplliifsvdgrasymkkgkvmnpnie 185

QY 191 KLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVDFATFHLRGKEF 250

Db 186 klrscgthspymrpvyptktfpnlytlatglypeshgi vgnsmypdvdfatfhlrgrekf 245

QY 251 NHRWGGQPLWTATKQGVKAGFFWSVWIPHERRIILTILRWLTLPDHERPSVYAFYSEQ 310

Db 246 nhrwggqplwtatkqgvkagffwsvipherriiltllqwlspnerpsvayafyseq 305

QY 311 PFGSGHKYGPFGFPESSYSGSPFPAKRPRKVKAPKRQERPVPAPPKRRRKIRHMDHYAA 370

Db 306 pfgsghkygpfpgpe----- 319

QY 371 ETRQDRMTNPLREIDKIVGQMDGLKQLKLRVCNVIFVGDHGMEDVTCRTFEFLSNLT 430

Db 320 -----mtnplreidktvgqlmdgklqrlhrvcnvifvgdhgm edvtcrtfe flsnlt 373

QY 431 NVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQHFEPYLOKHLRRLHYANN 490

Db 374 nvdditlvpgtlgrirskfsnna kydpkaiianltckkpdqhfkpymkqhlprlhyann 433

QY 491 RRIEDIHLLVERRHWVARKPLDYVKPSGKCFQGDHGFNDKNVSMQTVFVGYPGTFKYK 550

Db 434 rriedihllvdrwhvarkpldyvkpsgkcfqgdhgfndkvnsmqt vfvgygptfkyr 493

QY 551 TKVPPFENIELYNMCDLLGLKPAPNNGTHGSLNHLRTMTFRPTMPEEVTREPNYIGIMY 610

Db 494 tkvppfenielynmcdllglkpapnngthgslnhlrtmtfrptmpeevsrpnypgimy 553

QY 611 LQSDFDLGCTCDDKVEPKNKLDLNLKRLHTKSGTEERHLLYGRPAVLYRTYDILYHTDF 670

Db 554 lqsefdlgtctddkvepknkleeinlrhlthkgs teerhll ygrpavlyrtydydilyhtdf 613

QY 671 ESGYSIFLMLLWTSVTVSQAEVSSVPDHLTSCVRPDVRVSPFSQNLAYKNDKMSY 730

Db 614 esgysifimplwtstytskqae vssipehltn cvrpdvrsvgsfgsqnc laykndkmsy 673

QY 731 GLFPPYLSSEPEAKYDAFLVTNMVMPYPAFRKRWNYFORVLVKYASERGNVVISGPI 790

Db 674 glfppylsssepeakydaf lvtnmvmpy pafkrw yfqr vlvkkyaserngvnisgpi 733

QY 791 FDYDYGDLHDTEKIKQYVEGSSIPVPTHYYSITSCLDFTQADKCDGPLSVSSFFILPH 850

Db 734 fdynydgldrtdelkqyvegssipvthyysit scldftqadkcdgplsvssffilph 793

QY 851 RPDNEESCNSSDESKWVELMKMHTARVDRDIEHLTSLDFFRKTSRSYPIELTLKTYLHT 910

Db 794 rpdnescsnssedeskwveelmkmtarvdrdiehl tsgldy rkt rsyseil tltktylht 853

QY 911 YESEI 915

Db 854 yesei 858

RESULT 9

AAY71986

ID AAY71986 standard; Protein; 858 AA.

XX AC AAY71986;

XX DT 28-MAR-2001 (first entry)

XX DE Rat autotaxin protein.

XX KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;

XX KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;

XX KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;

XX KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;

XX KW type I phosphodiesterase activity; ATP pyrophosphatase activity;

XX KW ATPase; adenosine-5'-triphosphatase activity.

XX OS Rattus sp.

XX FH Key Location/Qualifiers

Domain 5..15
Binding-site /note= "Putative transmembrane domain"
122..124
Region /label= RGD_binding_domain
143..158
Region /label= Epitope
149..158
Region /note= "This region is specifically claimed in claim 10"
/label= Epitope
/note= "This region is specifically claimed in claim 10;
This region is absent in rat brain autotaxin designated
as PD-talpa sequence (AA71989)"
Active-site 196..208
Region /note= "Autotaxin phosphodiesterase catalytic site"
585..595
Region /label= Epitope
/note= "This region is specifically claimed in claim 10"
WO200068386-A1.
16-NOV-2000.
05-MAY-2000; 2000WO-US12402.
07-MAY-1999; 99US-0306979.
(ZYMO) ZYMOGENETICS INC.
Kelly JD;
WPI; 2001-007397/01.
N-PSDB; AAD02131.
New autotaxin proteins, useful e.g. for treating diabetes mellitus and
obesity, stimulate glucose uptake by cells and inhibit lipolysis -
Claim 1; Page 101-104; 126pp; English.
The present sequence is rat autotaxin protein. Autotaxin is a
glycoprotein cytokine which increases insulin
signalling in adipose tissue by producing substrate for adenosine
receptors, resulting in inhibition of lipolysis, decreased hepatic
gluconeogenesis and serum glucose levels, and increased insulin
sensitivity. It also inhibits differentiation of adipocytes.
Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
(ATPase) and ATP pyrophosphatase activities. Autotaxin and its
analogues are used to stimulate glucose uptake by cells, particularly
to reduce serum glucose levels for treatment of non-insulin dependent
diabetes (NIDDM) in humans, or generally any condition associated
with elevated serum levels of glucose, lipid or free fatty acid
(e.g. obesity or dyslipidemia). Transgenic animals that overexpress
autotaxin are models for human metabolic diseases.
Sequence 858 AA;

Query Match 88.2%; Score 4426.5; DB 22; Length 858;
Best Local Similarity 88.6%; Pred. No. 0;
Matches 802; Conservative 31; Mismatches 19; Indels 53; Gaps 2;

QY 14 QIISLFTAVGVISICLGFTHRIKRAEGWEGPPVVLSDSPWNTNSGCKGRCFELQEG 70
:::|||||: |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |
7 rvislftaivnlcglftasrikrae-wdegptvlslsdspwntntsgckgrcfelqevg 65
QY 71 PDCRCNDLKSYSCTCHDFDELCLKTARGWECTDRCGEVNEENACHCEDCLARGDC 130
|||||||: |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |
D6 pdcrcndlksysccchdfdelclktargwectdrdgevneenachcedclargdc 125
QY 131 CTNYGVCKGSHWDDCEETKAECPAGFVRPPLIIFSDGVFRASYMKKSKVMPNIE 190
|||||||: |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |
D6 ctnygvckgeshwddceelkpecpagfvrpplliifsvdgvfrasykmkkskvmnpnie 185
QY 191 KLKRCGTHSPYMRPVYPTKTFPNLTATGLYPESHGIVGNSWYDPVDFATFLHGREKF 250

Db 186 klrscgthapmrvpyptkftfnlytlatglypeshgivgnsmydvpfdasfhrgrk 245
QY 251 NHRWGGQPLWITATKOGVACAGTFFSWVIPHERRILTLRWLTPDHERSVYAFSEQ 310
|||||||: |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |
D6 nhrwggqplwitatkogvragtffswvipherriltilqwlalpdnerpsvafyse 305
QY 311 PDFSGHYGPGPESSVSGSPFTAKRPKRKVPKRQERVPAPPKRRRIHRMDHVA 370
|||||||: |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |
D6 306 pdfsgghygpfgpe ----- 319
QY 371 ETRODKMTNPLREIDKIVGQLMDGLKQLKRRCVNVIFVGDHGMEDVTCDRTELSNYLT 430
|||||||: |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |
D6 320 -----mtnplreidkvtgqlmdgkqlrlhrcvnlvifvgdhgmedvtcdrtfslnylt 373
QY 431 NVDDITLVPGTLGRIRSKFSNNAKYDPKAIITANITCKKPDQHPYKQLKHLPRKLUHANN 490
|||||||: |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |
D6 374 nvdditlvpgtlgriraksinnskydpkaiitankkpdqhpkykmlpkrlhyann 433
QY 491 RRIEDIHLLVERHVARVKPLDVYKPSGKCFQGDHGFNKNVSMQTVFVGYPGTFKYK 550
|||||||: |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |
D6 434 rriedihllvdrrwhvarvkpldvkykpsgkcfqgdhgfndknvsmqtcvfygypgtfkyr 493
QY 551 TKVPPFENIELYNVMDLGLKLPAPNNGTHGSLNHLRTNTFRPTMPEVTRPNYPGIMY 610
|||||||: |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |
D6 494 tkvppfenielynmcdlglkbpapnngthgslnhllrtntfrptmpdevsrpnypgimy 553
QY 611 LQSDFDLGCTCDDKVEPKNLDELKRLHTKSTGEERHLLYGRPAVLRYTRYDILYHTDF 670
|||||||: |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |
D6 554 lqsefdlgtctcdkvepknlleelnrlhtksgteerhlllygrpavlyrtsydylyhtdf 613
QY 671 ESGYSEIFLMLLWTSYTVSKOAEVSSVPDHLTSCVRDVRVSPFSQNCILAYKNDQMSY 730
|||||||: |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |
D6 614 esgyseiflmlwtsytiskvaevssipehltnrcvrdvrvspfsqncilaykndqmsy 673
QY 731 GFIFPPYLLSSSPKAYDAFLVTNNVMPYPAFKRVNMFQRLVKKYASERGVNVSQPI 790
|||||||: |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |
D6 674 gfifppylssspkaydavlvtmnmvmpafkrvayfqrvlvkkysasergvnvisgpi 733
QY 791 FDYDYGDLHDTEDKIQYVEGSSIPVTHYISITSLDFTQPADKCDGPLSVSFLPH 850
|||||||: |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |
D6 734 fdynydlrtdedeikyyvegssipvpthyysitclfdtqpadkcdgplsvsflph 793
QY 851 RPDNEESCNSDESKVVEELMKMHTARVDRDIEHLTSLDFPRKTSRSPYELLTKTYLHT 910
|||||||: |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |
D6 794 rpdndescnsedeskvwelkmhmtarvdrdiehlgtldfyrktsrspyseiltktylht 853
QY 911 YSEFI 915
D6 854 yesei 858
RESULT 10
AA71996
ID AA71996 standard; Protein; 858 AA.
XX
AC AA71996;
AC
XX
DT 28-MAR-2001 (first entry)
XX
DE Rat autotaxin variant (A194V).
XX
KW Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
KW adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic;
KW therapy; metabolic disease; obesity; dyslipidemia; serum glucose;
KW non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
KW type I phosphodiesterase activity; ATP pyrophosphatase activity;
KW ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.
XX
OS Rattus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers

PI Kelly JD;
XX WPI; 2001-007397/01.
XX New autotaxin proteins, useful e.g. for treating diabetes mellitus and
PT obesity, stimulate glucose uptake by cells and inhibit lipolysis -
PS Disclosure; Page -: 126pp; English.
XX
CC The present sequence is variant (A93V) of rat autotaxin protein.
CC Autotaxin is a glycoprotein cytokine which increases insulin
CC signalling in adipose tissue by producing substrate for adenosine
CC receptors, resulting in inhibition of lipolysis, decreased hepatic
CC gluconeogenesis and serum glucose levels, and increased insulin
CC sensitivity. It also inhibits differentiation of adipocytes.
CC Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase
CC (ATPase) and ATP pyrophosphatase activities. Autotaxin and its
CC analogues are used to stimulate glucose uptake by cells, particularly
CC to reduce serum glucose levels for treatment of non-insulin dependent
CC diabetes (NIDDM) in humans, or generally any condition associated
CC with elevated serum levels of glucose, lipid or free fatty acid
CC (e.g. obesity or dyslipidemia). Transgenic animals that overexpress
CC autotaxin are models for human metabolic diseases.
CC Note: The present sequence is not shown in the specification
CC but is derived from rat autotaxin protein sequence found in
CC page 101-104 of sequence listing (AAY71986).
XX
SQ Sequence 858 AA;

Query Match 88.1%; Score 4422.5; DB 22; Length 858;
Best Local Similarity 88.5%; Pred. No. 0;
Matches 801; Conservative 31; Mismatches 20; Indels 53; Gaps 2;

QY 11 QIISLTFVAVGVSICLGFATRIKRAEGWEGPPTVLSDSPWNTSGSGKRCFELQEAG 70
Db :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :
7 rvislftfaivsniclgftasirae-wdegptvlsdspwtntsgsgkrcfqlqevg 65
QY 71 PDCRCNLKSYNSCCHDFDELCLKTARGHECTKDRGEVNEENACHCEDCLARGDC 130
Db :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :
66 pdcrcnclksyscchdfdelclktvrgectkdrgevrneenachcsedclsrqdc 125
QY 131 CTNYQVYCKGSHWVDDCEIKAAECAPAGFVRPPLIIFSDGFRASYMKGSKVMPNTE 190
Db :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :
126 ctnyqvckgshwvddceieikvpecpagfvrpplifsvdgfrasymkvsgkvmnpnie 185
QY 191 KLRSCGTHSPYMRPVYPTKTPNNLYTLATGLYPESHGIVGNSMYDVFDPATHLRGREKF 250
Db :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :
186 klrscgthapymrpvyptktpnlytlatglypeshgivgnsmydpvdfdasfhlrgrekf 245
QY 251 NHRWGGOPWITATKGVKAGTFWSVVIPIHERRILITLRLWLTLPDHERPSVYAFYSEQ 310
Db :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :
246 nhrwggoplwitatkgvragtffwsvispherrilltilglwslpdrperpsvyafyseq 305
QY 311 PDFSGHKYGPPESSVSGSFPTAKRPRKRVAPRRQRPVAPPKRRKRTHRMDHYAA 370
Db :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :
306 pdfsgkhygpfge----- 319
QY 371 ETRODKMTNPLREIDKTVGLQMDGLKQLKRRVNVIFVGDHGMEDVTCDRTEFLSNLYLT 430
Db :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :
320 -----mtnplreldktvgldmglkqlhrcvnnvifvgdhgmvedvcdtrteflsnlylt 373
QY 431 NVDDITLVPGLGRISKFSNADYDKAIITANLTCKRPDQHFKPYLKHQLPKRLHYANN 490
Db :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :
374 nvdditlvpglgrisksinnskypdktiianltckpdkhfkpykqhlpkrlhyann 433
QY 491 RRIEDIHLLVRRHWARKPLDVYKKPSGKCFQGDHGFNDKVNMSQTVFVGYGPTFYK 550
Db :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :
434 rriedihllvrrhwarkpldvyykpsgkcfqgdhgfndkvnsmqtvfvygptfkyr 493
QY 551 TKVPPFENIELYNWCDLGLKLPAPNNGTHCSLNHLTLNTFRTPMPEVTRPNYPGIMY 610
Db :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :
494 tkvppfenielynwcdllglkppapnngthgslnhllrtntfrttmpdevsrpnypgimy 553

QY 611 LOSDFDLGCTCDDKVEPKNKLDLNLKRLHTKSGTERHLLYGRPAVLRYTRDYLYHTDF 670
Db :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :
554 lqsefdlgtctddkvepknkleeelnrlhktgsteerhlllygrpavlyrtsydylyhtdf 613
QY 671 ESGYSRIFLLMLTSTVSKOAEVSSVPDHLTSCVRPDVRVSPFSQNCCLAYKNDKQMSY 730
Db :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :
614 esgyseiflmltstvtiskvaevssipehltnrcvrdvrvspqfscnclaykndkqmsy 673
QY 731 GFLFPPYLSPPAKYDAFLVTNNVPMYPAFKRVWNTFORVLVKKYASERNGVNVISGPI 790
Db :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :
674 gflfppylsspeakydaflvtmvmmpafkrwafqrvlvkkyaserngvnavisgpi 733
QY 791 FDYDGLDHTEDKIKQYVSGSSIPVPTHYSIITSLDFTOPADKCDGPLSVSSFILPH 850
Db :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :
734 fdynygdrltdedekqyvegsslpvpthysiiitcltdftqpadkcdgplsvssfilph 793
QY 851 RPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSSRYSPEITLTLYLHT 910
Db :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :
794 rpdnesccnsedeskweelmkmtarvrdiehltdgldfyrktsrysteiltiktylht 853
QY 911 YESEI 915
Db :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :|||||: :
854 yesei 858

RESULT 12
AAR86595
ID AAR86595 standard; Protein; 849 AA.
XX
AC AAR86595;
XX
DT 01-JUL-1996 (first entry)
DE
DE N-tera 2D1 autotaxin protein.
KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMP;
KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.
XX Homo sapiens.
XX W09532221-A2.
XX
XX 30-NOV-1995.
XX 24-MAY-1995; 95WO-0506613.
XX 28-NOV-1994; 94US-0346455.
XX 25-MAY-1994; 94US-0249182.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Krutzy J, Liotta L, Murata J, Schiffmann E, Stracke M;
PI WPI; 1996-020533/02.
DR
XX Autotaxin motility stimulating protein, and DNA encoding it - used
PT in cancer diagnosis and therapy
PS Claim 4; Page 86-89; 112pp; English.
XX
CC AAR86559-R86596 represent autotaxin (ATX) and fragments of it. This
CC sequence represents the full length protein sequence of the
CC teratocarcinoma N-tera 2D1 ATX protein. ATX is an autocrine motility
CC stimulating protein which is present in cancer cells. ATX stimulates
CC both random and directed migration of melanoma cells. The tumorous
CC form of ATX is a secreted protein, while the transmembrane bound form is
CC not present in tumour cells. The cDNA encoding this sequence can be used
CC in a vector, to transform cells. The recombinant cells can then be used
CC to produce the peptide sequences. Antibodies specific for these
CC sequences can be produced, and can be used in cancer diagnosis and
CC therapy. Different sites of localisation of the protein are utilised for
CC diagnosis and prognosis of the stages of tumour progression. The

Db 1 marqcglsqfqlsftaisvniclftasrikrae-wdegpptvlsdpswntsgsk 59
Qy 61 GRCFELQAGPPDCRCDNLCKSTSCSHDDELCLKTARGWECTKRCGEVRNEENACHC 120
Db 60 grcfelqevgppdcrcdnlcksysscchdfclclktvrgwectkdrsevrneenachc 119
Qy 121 SEDCLARGDCCTNYQVVGKESHWD-----DCBEIKAAECPCAGFVRPPLLIIFSVDG 173
Db 120 pedclsrqdcctnyqvvckgeshwdaarnqsecqlqv-----cp-----ppllifsvdg 170
Qy 174 FRASYMKGSKVMPNIEKLKSCGTHSPYMPVPTTFPNLYTLATGLYPESHGIVGNSM 233
Db 171 frasymkgskvmpnieklrscgthpytpvpytktfpnlytlatgлыпeshgivgns 230
Qy 234 YDPVDFATHLRGREKFNHWGQGLWITATKQGVKAGTFFWSVVTPHERRILTIWL 293
Db 231 ydpvdfasfhlrgreknhrwggqplwitatkqvragnfwwsvsipherriltilql 290
Qy 294 TLPDHERPSVYAFYSEOPDFSGHKYGFPGPESSYSGSPFPAKRPRKRVAPKRQERPA 353
Db 291 slpdnerpsvayfseopdfsgkhypgfgpe----- 321
Qy 354 PPKRRRKIRHMDYAAETRQDKMTNPLREIKIVGQMDGLKQLKLRRCVNVIFVGDHG 413
Db 322 -----mtnplreiktvgqlmglkqlrhrvcnvifvgdhg 358
Qy 414 MEDVTCDRTEFISNLTNVDDITLVPCTGIRSKTSNNAKYDPKAIIANLTCKKPOHF 473
Db 359 medvtcdrtfislntnvdditlvpctgltgraksinnskypkttianltckkpdqhf 418
Qy 474 KPYLKOHLKRLHYANNRRTEDHLLVERWHVARKPLDVYKPSGKCFQGDHGFNDKV 533
Db 419 kpymkqhlprlhyannrriedhllvdrwhvarkpldvkykpsgkcfqgdhgfndkv 478
Qy 534 NSMQTVFGYGTFFKTKVPPENIELYNVMDLLGLKLPANNNGTHGSLNHLRTWTF 593
Db 479 nsmtvfygygtffktytkvpfenielynmcdllglkpapnngthgslnhlrtwtf 538
Qy 594 PTMPEVTRNPYGMVYLOSDFDLGCTDDKVEPKNKLDELNKLRLHTKGSTE----- 645
Db 539 ptmpevtrnpypgimylqsefalgctddkvepknkleeelnrlhtkkgsteaetgkfr 598
Qy 646 -----ERHLLYGRAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTV 688
Db 599 skhenknngsveprkerhllgrpavlyrtydydlyhtdfesgyseiflmpwtsyti 658
Qy 689 SKQAEVSSVPDHLTSCVRDPVRVSPFSONCLAYKNDQMSYGLFPPYLSSSPEAKYDA 748
Db 659 skqaevsvipelhtncvrpdrvrspfsqnclyakndqmsyglfppylssspeakyda 718
Qy 749 FLVTNMVMPYPAFRVWYFQRLVVKYASERNGVNVIISGPIFYDYGDLHDTEDKIQY 808
Db 719 flvtnmvmpyafkrwvayfqrllvkkyserngvnvisgpidynydlrdtedekiky 778
Qy 809 VEGSSIPVTHYISITSLDFTQPADKDGPLSVSSFILPHRPNDESCNSEDSEKWW 868
Db 779 vegssipvthyisitslclftqpadkdgplsvssfilphrpdndescnsedeskw 838
Qy 869 BELMKHTRARVDIEHLTSLDFFRKTSRSYVPELTILTKTYLHTVESEI 915
Db 839 eelmhtrarvdielhtgldfyrktsrsyvelitlkyhtyesei 885

RESULT 14

AAR86580
ID AAR86580 standard; Protein; 979 AA.
XX
AC AAR86580;
XX
DT 28-JUN-1996 (first entry)
XX
DE Autotaxin derived from human liver cells.

XX
KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
XX melanoma cell; tumour; antibody; cancer diagnosis; therapy.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 864 /note= "unspecified amino acid"
FT Misc-difference 889 /note= "unspecified amino acid"
FT Misc-difference 905 /note= "unspecified amino acid"
FT Misc-difference 911 /note= "unspecified amino acid"
FT Misc-difference 927 /note= "unspecified amino acid"
FT Misc-difference 937 /note= "unspecified amino acid"
FT Misc-difference 944 /note= "unspecified amino acid"
FT Misc-difference 950 /note= "unspecified amino acid"
FT Misc-difference 954 /note= "unspecified amino acid"
FT Misc-difference 967 /note= "unspecified amino acid"
FT Misc-difference 975 /note= "unspecified amino acid"
FT
FT W09532221-A2.
PN
PD 30-NOV-1995.
XX
PF 24-MAY-1995; 95WO-US06613.
XX
PR 28-NOV-1994; 94US-0346455.
PR 25-MAY-1994; 94US-0249182.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Krutzsch J, Liotta L, Murata J, Schiffmann E, Stracke M;
XX
DR WPT; 1996-020533/02.
XX
PT Autotaxin motility stimulating protein, and DNA encoding it - used
PT in cancer diagnosis and therapy
XX
PS Claim 4; Page 67-70; 112pp; English.
XX
CC AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is
CC an autocrine motility stimulating protein which is present in cancer
CC cells. ATX stimulates both random and directed migration of melanoma
CC cells. The tumorous form of ATX is a secreted protein, while the
CC transmembrane bound form is not present in tumour cells. The cDNA
CC encoding this sequence can be used in a vector, to transform cells. The
CC recombinant cells can then be used to produce the peptide sequences.
CC Antibodies specific for these sequences can be produced, and can be used
CC in cancer diagnosis and therapy. Different sites of localisation of the
CC protein are utilised for diagnosis and prognosis of the stages of tumour
CC progression. The sequences can be used in treatment methods to
CC advantageously block the activity of the secreted form of ATX, while
CC having little effect on the membrane form of ATX.
XX
SQ Sequence 979 AA;

Query Match 85.3%; Score 4279; DB 17; Length 979;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 805; Conservative 13; Mismatches 36; Indels 70; Gaps 8;
Qy 1 MARRSSFSQCOIISLFTFAVGVSICLGTATRIKRAEGWECPPVLSDPWTNIGSGCK 60
|||||

Db 300 yltvdditlvpgtlgrirskfsnnakypdkailanltckkpdqhfkyplkqhlprlhy 359
QY 488 ANNRIRIEDIHLVERRRHWARKPLDVTYKKPSGCKFFQGDHGFQDNKVNMSMQTVFVGYGPTF 547
Db 360 annrriedihllverrrhwarkpldvkykpsgnafsfrettafdnkvnsmqtfvfygypgptf 419
QY 548 KYTKVPPFENIELYNVMDLLGLKAPNNGTHGSLNHLRTNTFRPTMPPEVTRPNYPG 607
Db 420 kytkvppfenielynvmcdllglkpnngthfslnhllrtntfrptmpeevtrpnypg 479
QY 608 IMYLODFDLGCTCDDKVEPKNLDELNKLRLHTKSGTEERHLLYG-RPAVLRYRTYDILY 666
Db 480 imylqsdfdlgctcdkvepknlidelnkrllhtkgsteerhlllygdrpavlyrtrydily 539
QY 667 HTDFESGYSEIFLMLWTSTVSKOAEVSSVDPDHLTSCVRPDRVSPFSQNCCLAYKNDK 726
Db 540 htdefesgyseifimplwtstcvskaeqvssvpdhltscvrpdvrvspsfsgnclaykndk 599
QY 727 QMSYGFLEPPYLSSSPEAKYDAFLVTNMVPMYPAFKRYWNTYFQRLVVKKYASERNGVNI 786
Db 600 qmsyggllgppysspeakydaflvtnmvpmypafkrwnyfqrvlvkkyaserngvni 659
QY 787 SGPIFYDYDGLHDTEDKIKQYVEGSSIPVPTHYISITSCLDFTQPADKCDGPLSVSSF 846
Db 660 sgplfydydglhdtedkikqyvegssipvpthyysitscldftqpadkcdgplsvssf 719
QY 847 ILHRPDNEESCNSEDESKWVEELMKMHTARVRDIEHLTSLDFPRKTSRYPPEILLTKT 906
Db 720 ilhrpdneescnsedeskweelmkmhtarvrddiehltsldfprktsrypeilltk 779
QY 907 YLHTYSEI 915
Db 780 ylhtyesei 788

Search completed: July 19, 2001, 14:45:00
Job time: 208 sec